

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 18:20:14 ; Search time 24035 Seconds

(without alignments)
11858.273 Million cell updates/sec

Title: US-10-715-665-6

Perfect score: 5882

Sequence: 1 tcgcgcttctcgatgatgc.....tatcacgagggcccttcgtc 5882

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5882	100.0	5882	6	AX154501 Sequence
2	4617.2	78.5	5459	6	AX154499 Sequence
3	4190	71.2	5128	6	AX154497 Sequence
4	3713.6	63.1	6299	6	AX154584 Sequence
5	2793	47.5	5130	12	AF286076 Expression
6	2658.4	45.2	4276	6	AX154496 Sequence
7	2601.2	44.2	4282	6	AX154583 Sequence
8	2397.8	40.8	6050	6	CQ855138 Sequence
9	2333.2	39.7	7551	6	CQ795336 Sequence
10	2333.2	39.7	7551	6	CQ857240 Sequence
11	2290.6	38.9	6577	6	AX427812 Sequence
12	2283.4	38.8	6505	6	AX427777 Sequence
13	2283	38.8	6460	6	AX427796 Sequence
14	2281.8	38.8	9620	6	AX164579 Sequence
15	2281.8	38.8	9620	6	AX164581 Sequence
16	2280.4	38.8	6577	6	AX427813 Sequence
17	2278	38.7	5411	12	CV003687
18	2275.8	38.7	6438	6	AX427919 Sequence
19	2275.8	38.7	6577	6	AX427794 Sequence

20	2270.8	38.6	6473	6	AX427862	AX427862 Sequence
21	2269.2	38.6	6607	6	AX427770	AX427770 Sequence
22	2266	38.5	6486	6	AX427920	AX427920 Sequence
23	2263.6	38.5	6605	6	AX427867	AX427867 Sequence
24	2263.6	38.5	6605	6	AX427868	AX427868 Sequence
25	2262	38.5	6538	6	AX427795	AX427795 Sequence
26	2261.6	38.4	6608	6	AX427884	AX427884 Sequence
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28	2260.6	38.4	7178	6	CQ795334	CQ795334 Sequence
29	2260.6	38.4	7178	6	CQ867238	CQ867238 Sequence
30	2260	38.4	6602	6	AX427865	AX427865 Sequence
31	2259.8	38.4	6609	6	AX427846	AX427846 Sequence
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34	2256.6	38.4	6565	6	AR235454	AR235454 Sequence
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39	2251.4	38.3	6586	6	AX427890	AX427890 Sequence
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42	2248.4	38.2	6542	6	AX427861	AX427861 Sequence
43	2248.4	38.2	6610	6	AX427829	AX427829 Sequence
44	2248	38.2	6623	6	AX427860	AX427860 Sequence
45	2246.4	38.2	6626	6	AX427878	AX427878 Sequence

ALIGNMENTS

RESULT 1	AX154501	5882 bp	DNA	linear	PAT 22-JUN-2001
LOCUS	Sequence 6 from Patent WO0138358.				
DEFINITION	AX154501				
ACCESSION	AX154501.1				
VERSION	GI:14536111				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Selby, M.C., Glazer, E.C. and Houghton, M.C.				
TITLE	Hbv/hcv virus-like particle				
JOURNAL	Patent: WO 0138358-A 6 31-MAY-2001;				
CHIRON CORPORATION (US)					
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ORIGIN

Query Match 100.0%; Score 5882; DB 6; Length 5882;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	CAGCTTGTCTGTAAAGCGGATGCCGGGAGCAGACAAGCCGTCAGGCGCGCTCAGCGGGT	120
Db	61	CAGCTTGTCTGTAAAGCGGATGCCGGGAGCAGACAAGCCGTCAGGCGCGCTCAGCGGGT	120
Qy	121	TTGCGCGGTGTGCGGGCTTGGCTTAACTATGCGGCATCAGAGCAGATGTACTGAGAGTGC	180
Db	121	TTGCGCGGTGTGCGGGCTTGGCTTAACTATGCGGCATCAGAGCAGATGTACTGAGAGTGC	180
Qy	181	ACCATATGAAGCTTTTTCGAAAAAGCCTAGGCGCTCCAAAAAGCCCTCTCACTACTTCTGG	240
Db	181	ACCATATGAAGCTTTTTCGAAAAAGCCTAGGCGCTCCAAAAAGCCCTCTCACTACTTCTGG	240
Qy	241	AATAGCTCAGAGCGGAGGGCGCTCTGGCTCTGTCATAAATAAAAAAATTAGTCAGCCCA	300
Db	241	AATAGCTCAGAGCGGAGGGCGCTCTGGCTCTGTCATAAATAAAAAAATTAGTCAGCCCA	300
Qy	301	TGGGGCGGAGATCGGCGGAACCTGGGCGGGAGGGAATTATGGCTATTGGCCATTGCGCAT	360
Db	301	TGGGGCGGAGATCGGCGGAACCTGGGCGGGAGGGAATTATGGCTATTGGCCATTGCGCAT	360
Qy	361	ACGTTGTATCTATATCATATAATGTACATTTATATGGCTCATGTCCAAATATGACCGCCA	420
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Qy	421	TGTTGACATTGATTATGACTAGTTAATAGTAATAGTAATAGTAATAGTAATAGTAATAGTA	480
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Qy	481	AGCCCATATATGGAGTTTCGGGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCG	540
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Qy	661	CATCAAGTGTATCATATGCCAAGTCCGCGCCCTATTTGACGTCAATGACGTAATGSCCC	720
Db	661	CATCAAGTGTATCATATGCCAAGTCCGCGCCCTATTTGACGTCAATGACGTAATGSCCC	720
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Qy	841	TAGCGGTTTGACTCAGCGGGATTTCCAAAGTCTCCACCCCATTTGACGTCATTTGGAGTTTG	900
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Db	901	TTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATACCCCGCCCGTTGACG	960
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Db	1021	CGTCAGATTCGCTCGGAGCGCATCCACGCTGTTTTGACCTCCATAGAGACACCCGGAC	1080

Qy	1081	CGATCAGCCTCCGCGCGCGGAAACGGTGATTTGGAAACGGGAGATTCGCCGTGCCAAGAGT	1144
Db	1081	CGATCCAGCCTCCGCGCGCGGAAACGGTGATTTGGAAACGGGAGATTCGCCGTGCCAAGAGT	1140
Qy	1141	GAGTAAGTACCGCTATAGACTCTATAGSCACACCCCTTTGGCTCTTATGCAATGCTATA	1200
Db	1141	GAGTAAGTACCGCCTATAGACTCTATAGSGACACCCCTTTGGCTCTTATGCAATGCTATA	1200
Qy	1201	CTGTGTTTTGGCTTGGGCGCTATACACCCCGCTCCTTATGCTATAGGTGATGCTATAGCT	1260
Db	1201	CTGTGTTTTGGCTTGGGCGCTATACACCCCGCTCCTTATGCTATAGGTGATGCTATAGCT	1260
Qy	1261	TAGCCTATAGGTGGGTTATTGACCAATTATGACCACTCCCTTATTTGTFGACGATACTT	1320
Db	1261	TAGCCTATAGGTGGGTTATTGACCAATTATGACCACTCCCTTATTTGTFGACGATACTT	1320
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Db	1321	TCCATTACTAATCCATAACATGCTCTTTGGCCAACTATCTATTTGGCTATATGCCAA	1380
Qy	1381	TACTCTGTCTTCAGAGACTGACACGGACTCTGTATTTTTCAGAGATGGGTCCTATTAT	1440
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Db	1561	GGCGGAGCTTCCACATCCGAGCCCTCGTCCCATCCGTCAGCGGCTCATGGTCGCTCGGC	1620
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Db	1621	AGCTCCTTGCTCTTAACAGTGGAGGCGAGACTTTAGGCACAGCACAATGCCACCAACC	1680
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Db	1681	AGTGTGCGGACAAGGCGGTGGCGGTAGGGTATGTGTCCTGAATGAGCTCGAGATTGG	1740
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Db	1861	AGGCGAGTGTAAGTCTGAGCAGTACTCGTTGCTCCGCGCGCGCCACAGACATAATAGCT	1920
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VERSION AX154499.1 GI:14536109
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SOURCE other sequences; artificial sequences.
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REFERENCE 1
AUTHORS Selby, M.C., Glazer, E.C. and Houghton, M.C.
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CHIRON CORPORATION (US)
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ORIGIN

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ORGANISM
synthetic construct
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AUTHORS Hbv/hcv virus-like particle
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JOURNAL CHIRON CORPORATION (US)
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CDS
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RESULT 4
AX164584 LOCUS
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ACCESSION AX164584
VERSION AX164584.1 GI:14545518
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Coit, D.C., Medina-Selby, A.C., Selby, M.C. and Houghton, M.C.
TITLE Novel hcv non-structural polypeptide
JOURNAL Patent: WO 0138360-A 6 31-MAY-2001;
CHIRON CORPORATION (US)
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MEEC"
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Query Match

63.1%; Score 3713.6; DB 6; Length 6299;

Best Local Similarity 77.4%; Pred. No. 0; Matches 4876; Conservative 0; Mismatches 1004; Indels 420; Gaps 14;

QY	2	CGCGCTTTCCGTTGATGACGGTGAACAACTCTGACACATGCGAGTCCCGGAGACGGTCAAC	61	1021	GTCCAGATCCCTCGGAGACGCCATCCACGCTGTTTTCACCTCCATAGAAGACACCGGACC	1080
Db	1	CGCGCTTTCCGTTGATGACGGTGAACAACTCTGACACATGCGAGTCCCGGAGACGGTCAAC	60	1082	GATCCAGCTCCCGCGCGCGGAAACGGTGCATTTGGAACGGGATTCCTCCGTCGCAAGAGTG	1141
QY	62	AGCTTCTCTTAAGCGGATGCGCGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGT	121	1081	GATCCAGCTCCCGCGCGCGGAAACGGTGCATTTGGAACGGGATTCCTCCGTCGCAAGAGTG	1140
Db	61	AGCTTCTCTTAAGCGGATGCGCGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGT	120	1142	AGTAAAGTACCGCTATAGACTCTATAGGACACACCCCTTTGGCTCTTATGCTATGCTATAC	1201
QY	122	TGCGGGGTGTCGGGGTGGCTTAACCTATGCGGATCAGAGCAGATTTGCTAGAGTGCA	181	1141	AGTAAAGTACCGCTATAGACTCTATAGGACACACCCCTTTGGCTCTTATGCTATGCTATAC	1200
Db	121	TGCGGGGTGTCGGGGTGGCTTAACCTATGCGGATCAGAGCAGATTTGCTAGAGTGCA	180	1202	TGTTTTTGGCTTGGGGCTATACACCCCGCTCTTATGCTATGCTATGCTATGCTATGCTAT	1261
QY	182	CCATATGAAGCTTTTTCGAAAGCCCTAGGCTCCCAAAAAGCCCTCTCACTACTCTCTGGA	241	1201	TGTTTTTGGCTTGGGGCTATACACCCCGCTCTTATGCTATGCTATGCTATGCTATGCTAT	1260
Db	181	CCATATGAAGCTTTTTCGAAAGCCCTAGGCTCCCAAAAAGCCCTCTCACTACTCTCTGGA	240	1262	AGCTATAGTGTGGGTATTTGACCACTTATGACCACTCCCTTATTTGGTGACCATCTTT	1321
QY	242	ATAGCTCAGAGCGGAGCGGCTCGGCTCTGCTATGCTATGCTATGCTATGCTATGCTAT	301	1261	AGCTATAGTGTGGGTATTTGACCACTTATGACCACTCCCTTATTTGGTGACCATCTTT	1320
Db	241	ATAGCTCAGAGCGGAGCGGCTCGGCTCTGCTATGCTATGCTATGCTATGCTATGCTAT	300	1322	CCATTAATCCATTAATGCTCTTTGCGCACTATCTCTTATTTGGTGATATGCAAT	1381
QY	302	GGGGCGGAGATGGGGCGGAACTGGGCGGAGGGAATTTTGGCTATTTGGCTATTTGGCTAT	361	1321	CCATTAATCCATTAATGCTCTTTGCGCACTATCTCTTATTTGGTGATATGCAAT	1380
Db	301	GGGGCGGAGATGGGGCGGAACTGGGCGGAGGGAATTTTGGCTATTTGGCTATTTGGCTAT	360	1382	ACTCTGTCTTTCAGAGACTGACACCGACTCTGTATTTTACAGGATGGGGTCCATTTAT	1441
QY	362	CGTTGTATCTATATCATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT	421	1381	ACTCTGTCTTTCAGAGACTGACACCGACTCTGTATTTTACAGGATGGGGTCCATTTAT	1440
Db	361	CGTTGTATCTATATCATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT	420	1442	ATTACAAATTCACATATACAAACCGCTCCCGCTGCGCGCAGTCTTTTATTAACAT	1501
QY	422	GTGACATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT	481	1441	ATTACAAATTCACATATACAAACCGCTCCCGCTGCGCGCAGTCTTTTATTAACAT	1500
Db	421	GTGACATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT	480	1502	AGCGTGGATCTCCGACATCTCGGTPACGTGTTCCGGAATGCGGCTCTTCTCGGTAGCG	1561
QY	482	GCCATATATGAGTTCCGGTTTACATAAATGAGTAAATGAGTAAATGAGTAAATGAGTAAAT	541	1501	AGCGTGGATCTCCGACATCTCGGTPACGTGTTCCGGAATGCGGCTCTTCTCGGTAGCG	1560
Db	481	GCCATATATGAGTTCCGGTTTACATAAATGAGTAAATGAGTAAATGAGTAAATGAGTAAAT	540	1562	GGGAGCTTCCACATCCGAGCCCTGCTCCATCCGTCGAGCGCTCATGCTCGCTCGGCA	1621
QY	542	CCAAACGACCCCGCCATGACGTCAATGAGTAAATGAGTAAATGAGTAAATGAGTAAAT	601	1561	GGGAGCTTCCACATCCGAGCCCTGCTCCATCCGTCGAGCGCTCATGCTCGCTCGGCA	1620
Db	541	CCAAACGACCCCGCCATGACGTCAATGAGTAAATGAGTAAATGAGTAAATGAGTAAAT	600	1622	GCTCTTGTCTTAAAGTGAGGCGCAGACTTAGGCACAGCAATGCCACCAACACCA	1681
QY	602	GGACTTTCCATTTGACGTCAATGAGTAAATGAGTAAATGAGTAAATGAGTAAATGAGTAAAT	661	1621	GCTCTTGTCTTAAAGTGAGGCGCAGACTTAGGCACAGCAATGCCACCAACACCA	1680
Db	601	GGACTTTCCATTTGACGTCAATGAGTAAATGAGTAAATGAGTAAATGAGTAAATGAGTAAAT	660	1682	GTGTCGCGCAAGGCGGTGGGTAGGTAATGTTCTGAAATAGTCTCGGAGATTTGG	1741
QY	662	ATCAAGTATCATATGCAAGTCCCGCCCTTATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT	721	1681	GTGTCGCGCAAGGCGGTGGGTAGGTAATGTTCTGAAATAGTCTCGGAGATTTGG	1740
Db	661	ATCAAGTATCATATGCAAGTCCCGCCCTTATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT	720	1742	CTCGACCTGGACGAGATGGAAGCTTAAGCGCGGAGAGAGATGCGAGGAGCTG	1801
QY	722	CTTGGCATTTATGCCCCAGTACGACCTTACGGGACCTTCTTCTTCTTCTTCTTCTTCTTCTT	781	1741	CTCGACCTGGACGAGATGGAAGCTTAAGCGCGGAGAGAGATGCGAGGAGCTG	1800
Db	721	CTTGGCATTTATGCCCCAGTACGACCTTACGGGACCTTCTTCTTCTTCTTCTTCTTCTTCTT	780	1802	AGTTGTTGTTTCTGATAAGAGTCAAGAGTAACTCCCGTTCGCGTCTGTTAAACGGTGA	1861
QY	782	TATTAGTCACTGATTTACCATGCTGATGCGTTTGGCAGTACACCAATGGCGGTGGAT	841	1801	AGTTGTTGTTTCTGATAAGAGTCAAGAGTAACTCCCGTTCGCGTCTGTTAAACGGTGA	1860
Db	781	TATTAGTCACTGATTTACCATGCTGATGCGTTTGGCAGTACACCAATGGCGGTGGAT	840	1862	GGGCACTGTAGTCTGAGCAGTACTGCTGCTGCGCGCGGCCACAGACATTAATAGCTG	1921
QY	842	AGCGGTTTGACTCAACGGGATTTCCAAAGTCTCCACCCCTTATGAGTCAATGGAGTTTGT	901	1861	GGGCACTGTAGTCTGAGCAGTACTGCTGCTGCGCGCGGCCACAGACATTAATAGCTG	1920
Db	841	AGCGGTTTGACTCAACGGGATTTCCAAAGTCTCCACCCCTTATGAGTCAATGGAGTTTGT	900	1922	ACAGACTACAGACTTCTTCTTCCATGGTCTTTTCTGAGTCACTGCTGCTGCGAGCAAT	1981
QY	902	TTTGGCACCACCAATCAACGGGATTTCCAAAGTCTCCACCCCTTATGAGTCAATGGAGTTTGT	961	1921	ACAGACTACAGACTTCTTCTTCCATGGTCTTTTCTGAGTCACTGCTGCTGCGAGCTAA	1980
Db	901	TTTGGCACCACCAATCAACGGGATTTCCAAAGTCTCCACCCCTTATGAGTCAATGGAGTTTGT	960	1982	TCAGCAATCATGGATGCAATGAAGAGGGCTCTGCTGTGCTG-----	2027
QY	962	AAATGGCGGTAGCGGTGACGGTGGAGGTCTATATAGCAGAGCTCGTTTAGTGAAC	1021	1981	GATTTCCATCGCGCCCATCAGCGGTACGCCAGCAGCAAGGGGCTCTTAGGGTGC	2040
Db	961	AAATGGCGGTAGCGGTGACGGTGGAGGTCTATATAGCAGAGCTCGTTTAGTGAAC	1020	2028	-----CTGCTGTGTGAGCAGTCTTCTGTTCTG	2054
QY	1022	GTCCAGTCCCTGGAGACGCCATCCACGCTGTTTTCACCTCCATAGAAGACACCGGACC	1081	2041	ATAATCAACGACCTAACTGGCGGACAAAAACCAAGTGGAGGTGAGGTCCAGATTTGT	2100
Db				2055	CCAGCGCTAGCGAATC-----	2072
				2101	TCAACTGCTGCCAAAACCTTCTCGGCAACGTGCAATCAATGGGGTGTGCTGGAGTGTCTAC	2160

QY	2073	CACGTCACCGGGGAAGTGC	CGGCGCA	CAC	TGTGTCTGGA	TTTGT	AGCCTCCTCGCACCA	2132
Db	2161	CACGGGGCGGAAACGAGGA	CCATCGCGTCACCC	AAGGGTCTGTGTCA	TCCAGATGTATACC	2220		
QY	2133	GGCCCCAGCAGAACGT	-----	-----	-----	-----	CCAGCTCATCAACACCA	2166
Db	2221	AATGTAGACCAAGACCT	TGTGGGCTGCCCGCTTCG	CAAGGTACCGCGCTCA	TTCGACACC	2280		
QY	2167	AC-----	-----	GGCAGTTGGCACCTCA	ATAGCAGCGGCCCTG	2198		
Db	2281	TGCACTTGGGCTCCTCGG	ACCCTTACCTG	TCAAGAGGCACGCGGATGT	CATTC	CCGCTG	2340	
QY	2199	AACGTCAATGATAGCCT	CAACACCGGCTGTTGG	CAGGGCTTTTCTAT	CAACCAAGTTC	2258		
Db	2341	CGCCGGCGGGTGATAG	CAGGGG	CAGCTGTGTGCGCCCGGCCCA	TTTCTACTTTGAAA	2400		
QY	2259	AACCTTTACGGCTGCT	CTGTGAGAGCTAG	CAGAGCTGCCAGCCCTTA	CCGATTTTGACCA	2318		
Db	2401	GGCTCCTCGGGGGT	CCGCTGTTG-TGCC	CCCGGGGCA	CGCGTGGGCATATTTAGGGC	2459		
QY	2319	GGCTGGGGCCCTAT	CAGTTATG	CCAAACGGAAGCGGCC	CCGACACAGCGCCCTACTGCTGG	2378		
Db	2460	CGCGGTGTGCAC	CCGTGAGGTGGCTA	AGGCGGTG	GACTTTATCCCTGTGAGAACCTAGA	2519		
QY	2379	CACTACCCCCCAAA	CCCTTGCGGT-----	ATTGTGCCGCGGAAGAG	TGTGTGTGGT	2429		
Db	2520	GACAACCATGAGGT	CCCGGCTGTTTCA	CGGATAACTCTCTCC	ACAGTAGTGGCCCCAGAG	2579		
QY	2430	CCGGTATATTGCTT	CAC	TCCAGGCCCGTGTGTGG	GAACGACGACAGTCCGGGCGG	2489		
Db	2580	CTTCCAGGTGGCT	CACCTTCA	TGCTCCACAGGCAGCGG	CAAAAGCACAAAGTCCCGGC	2639		
QY	2490	CCCACTACAGCTGGGG	-----	-----	-----	-----	TGAAATGATACGGA	2521
Db	2640	TGCATATGCAGCT	CAGGGCTATA	AGGTGCTAGTACTCA	ACCCCTCTGTGCTGCAACACT	2699		
QY	2522	CGTCTGTGCTTAA	CAATAC	CGGCCACCGCTGGGCA	ATTGTTCCGTTGTACCTGGAT	2581		
Db	2700	GGGCTTTTGGTCTT	ACATG	TGCCAAGGCTCAT	TGGGATCGATCCTAACAT	CAGCACCGGGGT	2759	
QY	2582	GAACCTCAACT	-----	-----	-----	-----	-----	2591
Db	2760	GAGAACAAATTAC	ACTGGCAGCCCATCA	CGTACTCC	ACCTACGGCAAGTTCTTGGCGGA	2819		
QY	2592	-----	-----	GGATTCACCAAGTGT	CGGAGCGCC-----	-----	-----	2617
Db	2820	CGCGGGTGTCT	CGGGGGCGCTTAT	GACAATAATTTGTGA	CGAGTGCACACTCCACGGA	2879		
QY	2618	TCTTTGTGTATCGG	AGGGGGGCA	CAACCCCTGC	ATGCCCCCACTGATTCGCTCCG	2677		
Db	2880	TGCCACATCCATCT	TGGGCA	TTGGCACTGTCTTTGA	CCAAAGACAGAGACTCGGGGGGCGAG	2939		
QY	2678	CAAGCATCCGAG	CCACATAC	TCTCGGTGGGCTCGG	GTCCCTTGGATCAC	CCCCAGGTG	2737	
Db	2940	ACTGTTGTGTCT	CGCCACCGCC	ACCCCTCGGGCTCC	GTCACTGTGCCCCATCCCAACAT	2999		
QY	2738	CCTGTCGACTAC	CCGATATAGGCT	TTGGCATATC	CTTTGTATCCATCAACTAC	ACCATATT	2797	
Db	3000	CGAGGAGGTTGCT	CTGTCTCA	CCACCGGAGAGATCC	CTTTTTTACGGCAAGGCTATCC	CCCT	3059	
QY	2798	TAAATCAGGATGT	ACGTGGGAGGGT	TCGAACACAGGC--	TGGAAGCTGCTGCAACTGG	2855		
Db	3060	GGAAGTATCAAG	GGGGGAGACATCT	CACTCTGTCTATTTCA	AAAGAAGAGTGC	CGACGA	3119	
QY	2856	ACGGGGGGCGAA--	CGTTTGCATCTGGA	AGATAGGGACAG	GTCCGAGATCGATATGGAGA	2913		
Db	3120	ACTCGCGCAAG	CTGTGTGCA	TTGGCA	TCAA	TGCCGTG	3179	
QY	2914	ACATCATATCAG	GAATCCTAGGA	CCCCCTGCTGT	TACAGCGGGGGTTTTTCTTGTGA	2973		
Db	3180	CGTGTCCGTAT	CCCGAC	CGAGCGGATGTTGT	CGTGTGGGCAACCGATCC	CCCTCATGAC	3239	

Qy	2974	CAAGATCCTCAAAATACCGCAGAG-----TCTAGACTCGTGGGACTTCTCTC	3023
Db	3240	CGGCTATACCGGGGACTTCGACTCGGTGATAGACTGCAATACGTGTGTCA	3299
Qy	3024	AAATTTCTAGGGGATCTCCCGTGTGCTTTGGGCCAAAATTCGCAGTCCCAACTCCAAT	3083
Db	3300	CGAATTTGAGCCTTGACCTTACCTTACCAATTGAGACAATCACGCTCCCCAGATGCTGT	3359
Qy	3084	CACCTACCAACCTCCTGTCTCTCCAAATTTGTCTGGTTATCGCTGGATGTCTCGCGCGT	3143
Db	3360	CTCCCGCACTCAACGTCGGGGCAGGACTGCGAGGGGAAGCCAGGCACTCTACAGATTTGT	3419
Qy	3144	TTTATCATATTCCTCTTTCATCTGCTGCTATAGCTCATCTTCTTATTTGGTTCTTCTGGAT	3203
Db	3420	GGCACGGGGGAGCGGCCCTCCGCGCATGTTTCGACTCGTCCGCTCTCTGTGAGTGTCTATGA	3479
Qy	3204	TATCAAGGTATGTTGCCCGTTTCTCTCTAAATTCACAGGATCAACAACAACGACTGCGGA	3263
Db	3480	CGCAGGCTGTGCTTGATATGAGCTCACGCCGCCGAGACTACAGTTAGGCTACGAGCGTAT	3539
Qy	3264	CCATGCAAAACCTGCGACGACTCCTGTCTCAAGGCAACTCT-----	3302
Db	3540	CATGAACAACCCGGGGCTCCCGTGTGCCAGGACCATCTGAATTTTGGGAGGCGTCTT	3599
Qy	3303	---ATGTTTCCCTCATGTTGCTGTACAAACCTACCGATGGAAATTCACCTGTATTTCCC	3359
Db	3600	TACAGGCTCACTCATATAGATGCCCACTTCTATCCAGACAAGACAGAGTGGGAGAA	3659
Qy	3360	ATCCCATCGTCCCTGGGCTTTCGCAAAATACCTATGGAGTGGGCGCTCAGTCCGTTCTCT	3419
Db	3660	CCTTCTTACCTGGTAGCGTACCAAGCCACCGTGTGGCTAGGGCTCAAGCCCTCCCC	3719
Qy	3420	TGGCTCAGTTTACTAGTGCCATTTGTTCACTGTTGCTAGGGCTTTCCCCCACTGTTTG	3479
Db	3720	ATCGTGGGACCATGTGGAGTGTGTTGATTCGCTCAAGCCACCCCTCATGGGCCAAC	3779
Qy	3480	CTTTCACTATATGGATGATGTGGATATGGGGGCCAAGTCTGTACAGCATCGTGAATCCC	3539
Db	3780	ACCCCTGTATACAGACTGGGCGCTGTTTCAGAAATGAAATCACCTGACGCAACCCAGTCA	3839
Qy	3540	TTTATATACC-----	3547
Db	3840	CAAAATACATCATGACATGCAATGTCGGCCGACCTGGAGGTGCTCACGAGCACCTGGGTGCT	3899
Qy	3548	-----	3547
Db	3900	CGTTGGCGGCGTCTGTGCTGTTGGCCGCGTATTGCTCTCAACAGGCTGCGTGGTGCAT	3959
Qy	3548	-----GCTGTTACCAATTTTCTTTGCTCTGGGTATACATTTAAGAAATTCAGATCGAG	3602
Db	3960	AGTGGGAGGGTCTGTTGTCGGGAAGCGGCAATCATACCTGACAGGGAATGCTCTCTA	4019
Qy	3603	CAGTCTAGAAAGCGCGCCAAATATCAAGGATCCACTACGCTTAGAGCTCGCTGATC	3662
Db	4020	CCGAGATTCGATGAGATGGAAGAGTGCTAGSATCCACTACGCTTAGAGCTCGCTGATC	4079
Qy	3663	AGCCTCAGCTGCTCTTAGTTGTCAGCCCATCTGTTGTTGTCCTTCCCTCCCCCGTGCCTTC	3722
Db	4080	AGCCTCAGCTGCTGCTTCTAGTTGTCAGCCCATCTGTTGTTGTCCTTCCCTCCCCCGTGCCTTC	4139
Qy	3723	CTTGACCTGGAAAGTGCCACTCCCATGCTCTTTCTCTAAATAAAATCAGGAAATTCGATC	3782
Db	4140	CTTGACCTGGAAAGTGCCACTCCCATGCTCTTTCTCTAAATAAAATCAGGAAATTCGATC	4199
Qy	3783	GCATTGCTGAGTAGGTGCTATTCTATTCTGGGGGGTGGGGTGGGACAGCAAGAGG	3842
Db	4200	GCATTGCTGAGTAGGTGCTATTCTATTCTGGGGGGTGGGGTGGGACAGCAAGAGG	4259
Qy	3843	GGAGGATTGGGAGACAATAGCAGGCACTGTGGGAGCTCTTCCGCTTCTCGTCACTG	3902
Db	4260	GGAGGATTGGGAGACAATAGCAGGCACTGTGGGAGCTCTTCCGCTTCTCGTCACTG	4319
Qy	3903	ACTCGCTCGCTCGGTCTGCGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGGTAA	3962

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RESULT 5
AF286076
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AF286076 5130 bp DNA circular SYN 27-DEC-2000
Expression vector AF286076, complete sequence.

AF286076 GI:12034709

Expression vector AF286076
Expression vector AF286076
other sequences: artificial
sequences; vectors.
1 (bases 1 to 5130)
Arthos,J. and Mullins,J.I.
Multipurpose Eukaryotic Expression Vector
Unpublished

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1851 GTTGTATTCTGATAAGAGTCAGAGTTAACTCCGTTGCGGTGCTGTAAACGGTGGAGGC 1910
QY |||||
1866 AGTGTAGTCTGACAGTACTGCTGTCTGCGCGCGCCACACAGACATATAGCTGACAG 1925
Db |||||
1911 AGTGTAGTCTGACAGTACTGCTGTCTGCGCGCGCCACACAGACATATAGCTGACAG 1970
QY |||||
1926 ACTAAACAGACTGTTCTCTTTCCATGGGTCTTTTCTGCACTCACCGTCTGACGAAATCAA 1985
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QY |||||
1986 GCATCATGTATGCAATGAAGAGAGGCTCTGCTGTGCTGTGCTGTGCTGTGAGAGCTC 2045
Db |||||
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QY |||||
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Db |||||
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Db |||||
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QY |||||
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QY |||||
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Db |||||
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QY |||||
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Db |||||
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RESULT 6
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AX154496.1
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Sequence 1 from Patent WO0138358.
linear
PAT 22-JUN-2001
KEYWORDS

SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	Selby, M. C., Glazer, B. C. and Houghton, M. C.
TITLE	Hbv/hcv virus-like particle
JOURNAL	Patent: WO 0138358-A 1 31-MAY-2001;
FEATURES	CHIRON CORPORATION (US)
source	Location/Qualifiers 1..4276 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="plasmid pCMVII"
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Query Match	45.2%; Score 2658.4; DB 6; Length 4276;
Best Local Similarity	72.7%; Pred. No. 0;
Matches:42/5; Conservative	0; Mismatches 1; Indels 1606; Gaps 1;
Qy	1 TC CGCGGTTTCGGTGATGACGGTGAAGAACTCTCTGCACATGCAGCTCCCGGAGACGGTCA 60
Dd	1 TC CGCGGTTTCGGTGATGACGGTGAAGAACTCTCTGCACATGCAGCTCCCGGAGACGGTCA 60
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Dd	61 CAGCTTGTCTGAAGCGGATGCCGGAGCAGACAAGCCCGTCAGCGCGCTCAGCGGTG 120
Qy	121 TTGGCGGTGTCGGGCTCGCTTAACATATGCCGATCAGACAGATTGTACTGAGATGC 180
Dd	121 TTGGCGGTGTCGGGCTCGCTTAACTATATGCCGATCAGACAGATTGTACTGAGATGC 180
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Dd	181 ACCATATGAAGCTTTTTCGAAAGCCTTAGCGCTCCAAAAGAACCTCTCTCACTTCTGG 240
Qy	241 AATAGTCTCAGAGCCGAGCGGCTCGGCTCTGCATAAATAAAAAAATAGTCAGCCA 300
Dd	241 AATAGTCTCAGAGCCGAGCGGCTCGGCTCTGCATAAATAAAAAAATAGTCAGCCA 300
Qy	301 TGGGCGGAGATGGCGGAACTGGCGGGAGGGAATATTGGCTATTGGCCATTGGCAT 360
Dd	301 TGGGCGGAGAAATGGCGGAACTGGCGGGAGGGAATATTGGGCTATTGGCCATTGGCAT 360
Qy	361 ACCTGTGATCTATCATATATGTATCATTTATATTGGCTCATGTGCCAATATGACCGCA 420
Dd	361 ACCTGTGATCTATCATATATGTATCATTTATATTGGCTCATGTGCCAATATGACCGCA 420
Qy	421 TGTTGACATTTGATTTATGATAGTTATTAATAGTAATCAAATPACGGGTCAATTAGTTCA 480
Dd	421 TGTTGACATTTGATTTATGATAGTTATTAATAGTAATCAAATPACGGGTCAATTAGTTCA 480
Qy	481 AGCCCATATATGGAGTTCCGGGTACATTAACCTTAGCGTAAATGGCCCGCTGGCTGACC 540
Dd	481 AGCCCATATATGGAGTTCCGGGTACATTAACCTTAGCGTAAATGGCCCGCTGGCTGACC 540
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Dd	541 CCCAAGCA CCCCGCCCATGACGTCAATAATAGCGTATGTTCCCATAGTAACGCCAATA 600
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Dd	601 GGGACTTTCCATTTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTA 660
Qy	661 CATCAAGTGTATCATATGCCAAGTCCGCCCTTATGACGTCAATGACGGTAAATGGCCC 720
Dd	661 CATCAAGTGTATCATATGCCAAGTCCGCCCTTATGACGTCAATGACGGTAAATGGCCC 720
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Qy 2281 GGCTAGCCAGCTGCCAGCCCTTACCGAATTTGACGAGGCTGGGGCCCTATCAGTTATG 2340
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ORIGIN

Query Match 44.2%; Score 2601.2; DB 6; Length 4282;
Best Local Similarity 72.5%; Pred. No. 0;
Matches 4268; Conservative 0; Mismatches 8; Indels 1612; Gaps 5;

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Db	601	GGGACTTTCCATGAGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTA	660
Qy	661	CATCAAGTGTATCATATGCCAAGTCCGCCCTTATTTAGCGTCAATGACCGTAAATGGCCC	720
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Db	901	TTTTGSCACCAAAATCAACGGGACTTTCACAAATGTGCTAATAACCCCGCCCGTTGACG	960
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Db	1081	CGATCCAGCCTCCGGCGCGGAAACGGTGCATTGGAAACGGGATTCCTCGTGCAGAGT	1140
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Db	1141	GACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCTATATA	1200
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Qy	1260	TTAGCCTATAGGTGGGTTATTGACCATATTGACCACTCCCTATTGGTGACGATACT	1319
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VERSION CQ855138.1 GI:51510567
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Hooper,J.W., Schmaljohn,C.S. and Custer,M.
TITLE Dna vaccines against hantavirus infections
JOURNAL Patent: WO 2004058808-A 4 15-JUL-2004;
U.S. Army Medical Research Institute of Infectious Diseases
Department of the Army (US)

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Matches 3456; Conservative 0; Mismatches 1097; Indels 240; Gaps 16;
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QY 397 GGCTCATGTCCCAATATGACCGCCATTTGACATTTGATTTAGTACTAGTTATTAAATAGTAA 456
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1772	Qy	GGCAGCGGCAGAAAGATGACAGGCTGAGTTGGTGTGTAATTCGTATAAGAGTCAGAGGT	1831	Db	AACTCCCGTTGCCGTGCTGTTAAACGTTGGAGGCGAGTGTAGTCTGTAGCAGTACTCGTTGC
2702	Db	GGCAGCGGCAGAAAGATGACAGGCTGAGTTGGTGTGTAATTCGTATAAGAGTCAGAGGT	2761	Qy	AACTCCCGTTGCCGTGCTGTTAAACGTTGGAGGCGAGTGTAGTCTGTAGCAGTACTCGTTGC
1832	Qy	AACTCCCGTTGCCGTGCTGTTAAACGTTGGAGGCGAGTGTAGTCTGTAGCAGTACTCGTTGC	1891	Db	AACTCCCGTTGCCGTGCTGTTAAACGTTGGAGGCGAGTGTAGTCTGTAGCAGTACTCGTTGC
2762	Db	AACTCCCGTTGCCGTGCTGTTAAACGTTGGAGGCGAGTGTAGTCTGTAGCAGTACTCGTTGC	2821	Qy	TGCGCGCGCGCCACACAGACAATAATAGCTGACAGACTTAACAGACTGTTCCTTTCCATGGG
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Matches 3122; Conservative			
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Db	2832	CTGGCGGAAGTCTCTGTAGTGTCTGTTATTTCGCCGGCGTGCAGCGCGAAACCCACGT	2891
Qy	2078	CACCGGGGGAAGTGC CGGCCACACTGTCTGTGAATTTTGTAGCTCTCTCGCACACAGCGC	2137
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Query Match 39.7%; Score 2333.2; DB 6; Length 7551;
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RESULT 11

AX427812

LOCUS AX427812 6577 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 50 from Patent W00232943.

ACCESSION AX427812

VERSION AX427812.1 GI:21537899

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Huang, Y. and Nabel, G.J.

TITLE Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization

JOURNAL Patent: WO 0232943-A 50 25-APR-2002;

GOVERNMENT OF THE UNITED STATES (US)

LOCATION/Qualifiers

1. 6577

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/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="plasmid pVR1012x/s containing HIV genes"

ORIGIN

Query Match 38.9%; Score 2290.6; DB 6; Length 6577;

Best Local Similarity 68.9%; Pred. No. 0;

Matches 3636; Conservative 0; Mismatches 1139; Indels 502; Gaps 16;

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Db 61 CAGCTTGTCTGTAAAGCGGATGCCGGAGCAGACAAGCCCGT CAGGCGCGCTCAGCGGGTG 120

Qy 121 TTGGCGGGTGTCCGGGCTGGCTTTAACTATGCGGCATCAGAGCAGATTGTACTGAGATGC 180

Db 121 TTGGCGGGTGTCCGGGCTGGCTTTAACTATGCGGCATCAGAGCAGATTGTACTGAGATGC 180

Qy 181 ACCATATGAAGCTTTTTCGCAAAAGCCCTAGGCCTCCAAAAAGCCTCTCTCACTACTTCTGG 240

Db 181 ACCATATGAAGCTTTTTCGCAAAAGCCCTAGGCCTCCAAAAAGCCTCTCTCACTACTTCTGG 240

Qy 207 181 ACCATATGAAGCTTTTTCGCAAAAGCCCTAGGCCTCCAAAAAGCCTCTCTCACTACTTCTGG 207

Db 207 181 ACCATATGAAGCTTTTTCGCAAAAGCCCTAGGCCTCCAAAAAGCCTCTCTCACTACTTCTGG 207

Qy 241 AATAGCTCAGAGCGCGGCGCTCGGCCTCTGTCATAATAAAAAAATTTAGTCAGGCCA 300

Db 241 AATAGCTCAGAGCGCGGCGCTCGGCCTCTGTCATAATAAAAAAATTTAGTCAGGCCA 300

Qy 235 208 GATGCGTAGGAGAAATATACCGCATCAG----- 235

Db 235 208 GATGCGTAGGAGAAATATACCGCATCAG----- 235

Qy 301 TGCGCGGAGAAATGCGCGGAACTGGCGGGGAGGGAATTAATGGCTTAATGGCCATTGCAT 360

Db 236 236 -----ATTGGCTATTGGCCATTGCAT 256

Qy 361 AGTTGTATCTATATCATTAATATGTACATTTATATTGGCTCATGTCCTCAATATGACGCCA 420

Db 257 AGTTGTATCTATATCATTAATATGTACATTTATATTGGCTCATGTCCTCAATATGACGCCA 316

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Qy 481 AGCCCATATATGAGTTCGCGGTTACATAAATTTACGGTAAATGGCGCGCTCGGCTGACCG 540

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Qy	3881	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	3880
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Qy	3881	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	3880
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AX427777						
LOCUS						
DEFINITION	Sequence 15 from Patent WO0232943.					
ACCESSION	AX427777					
VERSION	AX427777.1 GI:21537864					
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences, artificial sequences.					
REFERENCE	1					
AUTHORS	Huang, Y. and Nabel, G.J.					
TITLE	Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization					

JOURNAL	Patent: WO 0232943-A 15 25-APR-2002;
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	Best Local Similarity 69.5%; Pred. No. 0;
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Db	1 TCSCGGGTTTCGGTGATGACGGGTGAAACCTCTTGACACATGACAGCTCCCGAGACGGTCA 60
Qy	61 CAGCTTGTCTGTAAAGCGGATGCCGGAGCAGACAAAGCCGTCAGGGGGCGTCAGCGGGTG 120
Db	61 CAGCTTGTCTGTAAAGCGGATGCCGGAGCAGACAAAGCCGTCAGGGGGCGTCAGCGGGTG 120
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[illegible]

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DEFINITION Sequence 1 from Patent WO0138360.
ACCESSION AX164579
VERSION AX164579.1 GI:14545513
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Coit, D.C., Medina-Selby, A.C., Selby, M.C. and Houghton, M.C.
TITLE Novel hev non-structural polypeptide
JOURNAL Patent: WO 0138360-A 1 31-MAY-2001;
CHIRON CORPORATION (US)
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Query Match 38.8%; Score 2281.8; DB 6; Length 9620;
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Matches 2292; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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ACCESSION AX164581
VERSION   AX164581.1 GI:14545515
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ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Coit,D.C., Medina-Selby,A.C., Selby,M.C. and Houghton,M.C.
TITLE     Novel hcv non-structural polypeptide
JOURNAL   Patent: WO 0138360-A 3 31-MAY-2001;
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ORIGIN

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Matches 2292; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Search completed: April 30, 2005, 05:45:05
Job time : 24242 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 18:19:56 ; Search time 2706 Seconds
(without alignments)

12867.671 Million cell updates/sec

Title: US-10-715-665-6

Perfect score: 5882

Sequence: 1 tcgcgcttcgtgatgac.....tatcacaggcccttcgtc 5882

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3713.6	63.1	6299	4	Aaf83669 HCV NS3A
5	2658.4	45.2	4276	5	AAD06790
6	2654.4	45.1	10263	12	AD104102
7	2601.2	44.2	4282	4	Aaf83668
8	2419.2	41.1	6236	10	ACC71561
9	2399.4	40.8	6050	3	AAA47797
10	2397.8	40.8	6050	12	ADK15555
11	2395.6	40.7	6148	10	ACC71544
12	2363	40.2	6258	10	ACC71554
13	2333.2	39.7	7551	12	AD172981
14	2321.4	39.5	7626	10	AD864206
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ALIGNMENTS

RESULT 1

AAD06793

ID AAD06793 standard; DNA; 5882 BP.

XX AAD06793;

XX 06-AUG-2001 (first entry)

XX Plasmid pCMV-II-E2661-SAG.

DE Virus-like particle; immunogen; hepatitis B virus surface antigen; HBsAg;

XX HBV; chimeric antigen; hepatitis C virus; HCV; virucide; vaccine;

KW plasmid pCMV-II-E2661-SAG; cyclic; circular; ds.

XX Human cytomegalovirus.

OS Homo sapiens.

OS Hepatitis C virus.

OS Hepatitis B virus.

OS Bos sp.

OS Unidentified.

OS Chimeric.

XX Key

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FT domain"

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FT /note= "661 E2 coding sequence from HCV"

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FT 2907..3587

FT /tag= c

FT /note= "HBsAg S domain coding sequence from HBV"

FT WO200138358-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032249.

XX 24-NOV-1999; 99US-0167224P.

XX (CHIR) CHIRON CORP.

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AAD06792 ID AAD06792 standard; DNA; 5459 BP.
XX AAD06792;
XX
DT 06-AUG-2001 (first entry)


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XX Plasmid pCMVII opti 330 E1/SAg.
DE Virus-like particle; immunogen; hepatitis B virus surface antigen; HBsAg;
KW HBV; chimeric antigen; hepatitis C virus; HCV; virucide; vaccine;
KW plasmid pCMVII opti 330 E1/SAg; cyclic; circular; ds.
XX
OS Human cytomegalovirus.
OS Homo sapiens.
OS Hepatitis C virus.
OS Hepatitis B virus.
OS Bos sp.
OS Unidentified.
OS Chimeric.
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XX 31-MAY-2001.
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XX 22-NOV-2000; 2000WO-US032249.
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XX 24-NOV-1999; 99US-0167224P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Selby M, Glazer E, Houghton M;
XX
XX WPI; 2001-367661/38.
XX P-PSDB; AAE02621.
XX
XX Virus-like particle for use as an immunogen, comprising a first hepatitis
PT B virus surface antigen (HBsAg) and chimeric antigen comprising a second
PT HBsAg covalently linked to hepatitis C immunogenic polypeptide.
XX
XX Claim 33; Fig 3; 115pp; English.
XX
XX The invention relates to a virus-like particle for use as an immunogen,
CC comprising a first hepatitis B virus surface antigen (HBsAg) and a
CC chimeric antigen comprising a second HBsAg which is covalently linked to
CC an hepatitis C virus (HCV) immunogenic polypeptide, where the first and
CC the second HBsAg each comprise a substantially complete S domain. The
CC virus-like particle is useful as immunogen and as vaccine. The present
CC sequence is plasmid pCMVII opti 330 E1/SAG containing coding sequences
CC for 330 E1 envelope glycoprotein of HCV and S domain of HBsAg inserted
CC into pCMVII. The plasmid pCMVII is a pUC19-based cloning vector designed
CC for expression in mammalian cells. It comprises human cytomegalovirus
CC (CMV) immediate early (IE) enhancer/promoter, human CMV intron A, a human
CC tissue plasminogen activator (tPA) leader, a bovine growth hormone poly A
CC terminator (BGHT), a ColEI origin of replication and an ampicillin
CC resistance (Amp R) gene. The pCMVII opti 330 E1/SAG plasmid is used for
CC production of virus-like particle of the invention
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Best Local Similarity 89.1%; Pred. No. 0;
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QY 2881 AAGATAGGACAGGTCGAGATCGATATGGAGAAATCATCATCAGAGTTCTCTAGGACCCC 2940
DB |||||
QY 2465 -----GAACTGGAGCCCCACCAATGGAGAAATCATCATCAGAGTTCTCTAGGACCCC 2517
DB |||||
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DB |||||
QY 2638 ATTGCGAGTCCCCCAACTCCAAATCACTCACACCTCTCTCTCTCTCTCTCTCTCTCTCT 2697
DB |||||
QY 3121 ATGCTGTGATGTCTGCGCGGTTTTTATCATATTTCTCTCTCTCTCTCTCTCTCTCTCTCT 3180
DB |||||
QY 2698 ATGCTGTGATGTCTGCGCGGTTTTTATCATATTTCTCTCTCTCTCTCTCTCTCTCTCT 2757
DB |||||
QY 3181 TCTCTTATTGGTCTTCTGGAATTATCAAGGATGTTGGCCGTTTGTCTCTTAATTCAG 3240
DB |||||
QY 2758 TCTCTTATTGGTCTTCTGGAATTATCAAGGATGTTGGCCGTTTGTCTCTTAATTCAG 2817
DB |||||
QY 3241 GATCAACAAACCACTAGCGGACCATGAAACCTGCAACCTGCTGCTCAAGGCAACT 3300
DB |||||
QY 2818 GATCAACAAACCACTAGCGGACCATGAAACCTGCAACCTGCTGCTCAAGGCAACT 2877
DB |||||
QY 3301 CTATGTTTCCCTCATCTGTGCTGTACAAAACCTACGGATGGAAATTCACCTGTATTCCCA 3360
DB |||||


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QY 5521 GATCTTACCGCTGTTGAGATCCAGTTTCGATGTAACCCACTCGTGCAACCCAACTGATCTTC 5580
DB |||||
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DB |||||
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DB |||||
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DB |||||
QY 5641 AAAAAAGGGAATAAGGCGGACGCGCAAAATGTTCAATCTACTCTTCTCTTTTCAATA 5700
DB |||||
QY 5218 AAAAAAGGGAATAAGGCGGACGCGCAAAATGTTCAATCTACTCTTCTCTTTTCAATA 5277
DB |||||
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DB |||||
QY 5278 TTATTGAAGCATTTATCAGGGTTATTGTTCTCATGAGGGATACATATTTGAATGATTTTA 5337
DB |||||
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DB |||||
QY 5338 GAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAAGTGCCACCTGACGCTTA 5397
DB |||||
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DB |||||
QY 5398 AGAAACCATTTATTCATGACATTAACCTATAAAAAATAGCGGTATCACGAGGCCCTTTTCG 5457
DB |||||
QY 5881 TC 5882
DB ||
QY 5458 TC 5459
DB ||

RESULT 3
AAD06791
ID AAD06791 standard; DNA; 5128 BP.
AC
XX
AC AAD06791;
XX
DT 06-AUG-2001 (first entry)
XX
DE Plasmid pCMVII-ps2-SAG.
XX
KW Virus-like particle; immunogen; hepatitis B virus surface antigen; HBsAg;
KW HBV; chimeric antigen; hepatitis C virus; HCV; virucide; vaccine;
KW plasmid pCMVII-ps2-SAG; cyclic; circular; ds.
XX
OS Human cytomegalovirus.
OS Homo sapiens.
OS Hepatitis B virus.
OS Bos sp.
OS Unidentified.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 1988. .2833
FT CDS /*tag= a
FT /*product= "pres2 and S domains of HBsAg"
FT misc_feature 1988. .2152
FT /*tag= b
FT /*note= "pres2 domain coding sequence"
FT misc_feature 2153. .2833
FT /*tag= c
FT /*note= "S domain coding sequence"
XX
XX WO200138358-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 22-NOV-2000; 2000WO-US032249.
XX
XX 24-NOV-1999; 99US-0167224P.
FR (CHIR ) CHIRON CORP.
XX
XX Selby M, Glazer E, Houghton M;
PI
XX
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DR
DR WPI; 2001-367661/38.
XX P-PSDB; AAS02620.
PT Virus-like particle for use as an immunogen, comprising a first hepatitis
PT B virus surface antigen (HBsAg) and chimeric antigen comprising a second
PT HBsAg covalently linked to hepatitis C immunogenic polypeptide.
XX
PS Example 2; Fig 2; 115pp; English.
XX
CC The invention relates to a virus-like particle for use as an immunogen,
CC comprising a first hepatitis B virus surface antigen (HBsAg) and a
CC chimeric antigen comprising a second HBsAg which is covalently linked to
CC an hepatitis C virus (HCV) immunogenic polypeptide, where the first and
CC the second HBsAg each comprise a substantially complete S domain. The
CC virus-like particle is useful as immunogen and as vaccine. The present
CC sequence is plasmid pCMVII-ps2-SAG containing coding sequences for pres2
CC and S domains of HBsAg inserted into pCMVII between human cytomegalovirus
CC (CMV) intron A and bovine growth hormone poly A terminator (BGHT). The
CC plasmid pCMVII is a pUC19-based cloning vector designed for expression in
CC mammalian cells. It comprises human cytomegalovirus (CMV) immediate early
CC (IE) enhancer/promoter, human CMV intron A, a human tissue plasminogen
CC activator (tPA) leader, a bovine growth hormone poly A terminator (BGHT),
CC a ColEI origin of replication and an ampicillin resistance (Amp R) gene.
CC The pCMVII-ps2-SAG plasmid is used for production of virus-like particle
CC of the invention
XX
SQ Sequence 5128 BP; 1218 A; 1321 C; 1249 G; 1340 T; 0 U; 0 Other;
Query Match 71.2%; Score 4190; DB 5; Length 5128;
Best Local Similarity 85.7%; Pred. No. 0;
Matches 5038; Conservative 0; Mismatches 90; Indels 754; Gaps 4;
QY 1 TCGCGCGTTTCGGTGATGACGCGTGAACCTCTGACACATGAGCTCCCGGAGACGGTCA 60
DB 1 TCGCGCGTTTCGGTGATGACGCGTGAACCTCTGACACATGAGCTCCCGGAGACGGTCA 60
QY 61 CAGCTTGCTCTGAACGGATGCCGGGAGCAGACACAGCCGTCAGGCGCGTCAGCGGGTG 120
DB 61 CAGCTTGCTCTGAACGGATGCCGGGAGCAGACACAGCCGTCAGGCGCGTCAGCGGGTG 120
QY 121 TTGGCGGGGTGTCGGGGCTGGCTTAATCTATCGCGCATCAGACGAGATTGTACTGAGAGTGC 180
DB 121 TTGGCGGGGTGTCGGGGCTGGCTTAATCTATCGCGCATCAGACGAGATTGTACTGAGAGTGC 180
QY 181 ACCATATGAAGCTTTTTCGAAAAGCCTAGGCTTCCAAAAAGCCTCTCACTACTTCTGG 240
DB 181 ACCATATGAAGCTTTTTCGAAAAGCCTAGGCTTCCAAAAAGCCTCTCACTACTTCTGG 240
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DB 241 AATAGCTCAGAGCGCGAGCGGCGCTCGGCTCTGCATTAATAAAAAAATTTAGTCAGCCA 300
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DB 301 TGGGCGGAGAAATGGCGGAACTGGGCGGGGAGGGAATTTATGGCTATTGGCCATTGCGAT 360
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DB 421 TGTGTGACATTGATTATTGACTAGTTATTAAATAGTAAATACAGGGGTCATTAGTTTCAT 480
QY 481 AGCCCATATATGGAGTTCGCGGTTACATAAATTTACGTTAAATGGCCCGCTGGCTGACCG 540
DB 481 AGCCCATATATGGAGTTCGCGGTTACATAAATTTACGTTAAATGGCCCGCTGGCTGACCG 540
QY 541 CCCAACGACCCCCCGCCATTGACGTCATTAATGACGATGTGTTCCCAATAGTAACGCCAATA 600
DB 541 CCCAACGACCCCCCGCCATTGACGTCATTAATGACGATGTGTTCCCAATAGTAACGCCAATA 600
QY 601 GGGACTTTTCCATTGACGTCATTAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTA 660
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Db 601 ||||| GGGACTTTCCATTGACGCTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTGGCAGTA 660
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Qy 721 GCCTGGCATTTATGCCCAATGATACATGACCTTACGGGACTTTCTACTTGGCAGTAGTACATCTAC 780
Db 721 GCCTGGCATTTATGCCCAATGATACATGACCTTACGGGACTTTCTACTTGGCAGTAGTACATCTAC 780
Qy 781 GTATTAGTCAATCGTATTAATCATGTTGATCGGGTTTGGCAGTACACCAATGGGCGTGA 840
Db 781 GTATTAGTCAATCGTATTAATCATGTTGATCGGGTTTGGCAGTACACCAATGGGCGTGA 840
Qy 841 TAGCGGTTTCACTACACGGGATTTCCAAAGTCTCCACCCCAATGACGTCATGGGAGTTTG 900
Db 841 TAGCGGTTTCACTACACGGGATTTCCAAAGTCTCCACCCCAATGACGTCATGGGAGTTTG 900
Qy 901 TTTTGGCACCACCAATCAACGGGACTTTTCCAAATGTCTGTAATAACCCCGCCCGTTGACG 960
Db 901 TTTTGGCACCACCAATCAACGGGACTTTTCCAAATGTCTGTAATAACCCCGCCCGTTGACG 960
Qy 961 CAAATGGGCGGTAGGCGTGTACCGTGGAGGTCTATATAAGCAGAGCTCGTTTGTAGTGAAC 1020
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Qy 1021 CGTCAGATCGCTGGAGACGCCATCCACGCTGTTTGGACCTCCATAGACACACCGGAC 1080
Db 1021 CGTCAGATCGCTGGAGACGCCATCCACGCTGTTTGGACCTCCATAGACACACCGGAC 1080
Qy 1081 CGATCCAGCTCCCGGCGCGGAAACGGTGCATTTGGAAACGGGATTTCCCGTGCACAGAT 1140
Db 1081 CGATCCAGCTCCCGGCGCGGAAACGGTGCATTTGGAAACGGGATTTCCCGTGCACAGAT 1140
Qy 1141 GACGTAAGTACCGCTATAGACTCTATPAGGACACACCCCTTTGGCTCTTATPAGTATATA 1200
Db 1141 GACGTAAGTACCGCTATAGACTCTATPAGGACACACCCCTTTGGCTCTTATPAGTATATA 1200
Qy 1201 CTGTTTTGGCTTTGGGCGCTATACACCCCGCTCTTATGCTATAGTGTATAGTATAGCT 1260
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Qy 1261 TAGCTATAGGTGGGTATTTGACCACTATTGACCACTCCCTATTGGTGACGACTTT 1320
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Qy 1381 TACTCTGCTTTCAGAGACTGACACGGACTCTGTATTTTACAGGATGGGCTCATTTAT 1440
Db 1381 TACTCTGCTTTCAGAGACTGACACGGACTCTGTATTTTACAGGATGGGCTCATTTAT 1440
Qy 1441 TATTTACAAATTCACATATACAAACACCGCTCCCGTCCCGCAGTCTTTTATTAACA 1500
Db 1441 TATTTACAAATTCACATATACAAACACCGCTCCCGTCCCGCAGTCTTTTATTAACA 1500
Qy 1501 TAGCGTGGGATCTCCGACTCTCGGTAAGTGTTCGGGACATGGGCTCTTCCCGTAGC 1560
Db 1501 TAGCGTGGGATCTCCGACTCTCGGTAAGTGTTCGGGACATGGGCTCTTCCCGTAGC 1560
Qy 1561 GCGGAGCTTCCACATCCGAGCCCTGGTCCCATCGTCCAGCGGCTCATGGCTCGGC 1620
Db 1561 GCGGAGCTTCCACATCCGAGCCCTGGTCCCATCGTCCAGCGGCTCATGGCTCGGC 1620
Qy 1621 AGCTCTTGTCTCTAACAGTGGAGGCCAGACTTAGGCACAGCAATGCCACACACC 1680
Db 1621 AGCTCTTGTCTCTAACAGTGGAGGCCAGACTTAGGCACAGCAATGCCACACACC 1680
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Db 1681 AGTGTCCGCAAGGCGGTAGGGTATGTGTCTGAAATGAGCTCGGAGATTGG 1740
Qy 1741 GCTCGCACCTGGACGAGAGTAAAGCACTTAAGCAGCGGAGAGAGATGCGGCGAGCT 1800
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Qy 1861 AGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTCGCGGCGCGCCACAGACATAATAGCT 1920
Db 1861 AGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTCGCGGCGCGCCACAGACATAATAGCT 1920
Qy 1921 GACAGACTAACAGACTGTTCTTCCATGGGTCTTTTCTGCACTCACCGCTGTCGACGAA 1980
Db 1921 GACAGACTAACAGACTGTTCTTCCATGGGTCTTTTCTGCACTCACCGCTGTCGACGAA 1980
Qy 1981 TTTCAAGCAATCATGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGGAG 2040
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Qy 2041 CAGTCTTGTGTTGCGCCAGCGCTAGCGAAACCCACGTCACCGGGGAAAGTGCAGGCGACA 2100
Db 1999 CTCCACTGCTTCCACCAAACTCTGAGGATCCAGAGTCAGGGGTCTGTATCTTCTCTGC 2058
Qy 2101 CTGTGCTGGATTGTTAGCTCTCTCGCACCAGCGGCGCAAGCAGACGTCAGTGATCA 2160
Db 2059 TGGTGGCTC----- 2067
Qy 2161 ACACCAACGCGAGTTGGCACCTCAATAGCACGGCCCTGAACTGCAATGATAGCTCAACA 2220
Db 2068 -----CAGTTTCAGGAAACAGTAAACCTGCTCCGAAATTTGCT 2105
Qy 2221 CCGGCTGGTTGGCAGGGCTTTTCTATCAACAAGTTCAACTCTTCAGGCTGCTCTGAGA 2280
Db 2106 ----- 2105
Qy 2281 GGCTAGCCAGCTGCGACCCCTTACCGATTTTGACCAAGGCTCGGGCCCTATCAGTTTATG 2340
Db 2106 -----CTCACATCTGCTCAATCTCCGCGAGGACTGGGACC 2141
Qy 2341 CCNACGGAAGCGGCCCCGACCGCCCTACTGCTGGCACTACCCCCCAAAACCTTTGCG 2400
Db 2142 ----- 2141
Qy 2401 GTATTGTCCCGGAAGAGTGTGTGTGGTCCGGTATATTGCTTCACTCCAGCCCCGTGG 2460
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Db 2142 ----- 2141
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Db 2142 ----- 2141

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Db	2142	-----	2141
QY	2881	AAGATAGGACAGGTCCGAGATCGATATGAGAACATCATCAGGATTCCTAGGACCCC	2940
Db	2142	-----	2141
QY	2941	TGCTCGTGTACAGCGGGGTTTTCTTGTGTGACAAGATCCCTCACAAATACCGCAGAGTC	3000
Db	2187	TGCTCGTGTACAGCGGGGTTTTCTTGTGTGACAAGATCCCTCACAAATACCGCAGAGTC	2246
QY	3001	TAGATCGTGGTGGACTTCTCTCAATTTCTAGGGGATCTCCGCTGTGTTGGCCAAA	3060
Db	2247	TAGACTCGTGGTGGACTTCTCTCAATTTCTAGGGGATCTCCGCTGTGTTGGCCAAA	2306
QY	3061	ATTGCGAGTCCCAACCTCCAACTCACTCACCAACCTCCCTGCTCCAAATTTGTCCTGGTT	3120
Db	2307	ATTGCGAGTCCCAACCTCCAACTCACTCACCAACCTCCCTGCTCCAAATTTGTCCTGGTT	2366
QY	3121	ATCGCTGGATGTCTGCGCGTTTTATCATATTTCTCTTTCATCTGCTGCTATGCTCA	3180
Db	2367	ATCGCTGGATGTCTGCGCGTTTTATCATATTTCTCTTTCATCTGCTGCTATGCTCA	2426
QY	3181	TCCTCTTATTTGGTTCTTCTGGATATCAAGGTATGTTGCGGTTGTCCTCTAATTTCCAG	3240
Db	2427	TCCTCTTATTTGGTTCTTCTGGATATCAAGGTATGTTGCGGTTGTCCTCTAATTTCCAG	2486
QY	3241	GATCAACAACAAACAGTACGGGACCATGCAAAACCTGCAGACTCTGCTCAAGGCAACT	3300
Db	2487	GATCAACAACAAACAGTACGGGACCATGCAAAACCTGCAGACTCTGCTCAAGGCAACT	2546
QY	3301	CTATGTTTCCCTCATGTGCTGTACAAAACCTACGGATGGAATTGCACTGTATTTCCCA	3360
Db	2547	CTATGTTTCCCTCATGTGCTGTACAAAACCTACGGATGGAATTGCACTGTATTTCCCA	2606
QY	3361	TCCCATCGCTCGGGCTTTTCGAAAATACCTATGGAGTGGGCTCAGTCCGTTCTCTTT	3420
Db	2607	TCCCATCGCTCGGGCTTTTCGAAAATACCTATGGAGTGGGCTCAGTCCGTTCTCTTT	2666
QY	3421	GGCTCAGTTTACTAGTGCCATTTGTTTCAGTGGTTTCTGAGGGCTTTCCCCACCTGTTTGGC	3480
Db	2667	GGCTCAGTTTACTAGTGCCATTTGTTTCAGTGGTTTCTGAGGGCTTTCCCCACCTGTTTGGC	2726
QY	3481	TTTTCAGCTATATGGATGATGTGTTATTTGGGGCCAAAGTCTGTACAGCATCGTAGTCCCT	3540
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QY	3541	TTATACCGCTGTTACCAATTTCTTTTGTCTCTGGGTATACATTTAAGAAATTCAGACTCG	3600
Db	2787	TTATACCGCTGTTACCAATTTCTTTTGTCTCTGGGTATACATTTAAGAAATTCAGACTCG	2846
QY	3601	AGCAAGTCTAGAAAGCGGCCAAGATATCAAGGATCCACTACGCGTTAGAGCTCGCTGA	3660
Db	2847	AGCAAGTCTAGAAAGCGGCCAAGATATCAAGGATCCACTACGCGTTAGAGCTCGCTGA	2906
QY	3661	TCAGCCTCGACTGTGCCCTTCTAGTTGCGAGCCATCTGTTGTTTGGCCCTCCCGCTGCCT	3720
Db	2907	TCAGCCTCGACTGTGCCCTTCTAGTTGCGAGCCATCTGTTGTTTGGCCCTCCCGCTGCCT	2966
QY	3721	TCCTTGAACCTGGAAAGGTGCACCTCCCACTGCTCTTTCTTCTTAATAATGAGGAAATTCGA	3780
Db	2967	TCCTTGAACCTGGAAAGGTGCACCTCCCACTGCTCTTTCTTCTTAATAATGAGGAAATTCGA	3026
QY	3781	TCCATTTGCTGAGTAGTGTCTATTTCTGCGGGGTTGGGTGGGGAGGACAGCAAG	3840
Db	3027	TCCATTTGCTGAGTAGTGTCTATTTCTGCGGGGTTGGGTGGGGAGGACAGCAAG	3086
QY	3841	GGGGAGGATTTGGGAAGACAATAGCAGGATGCTGGGGAGCTCTTCGCTTCTCGCTCAC	3900
Db	3087	GGGGAGGATTTGGGAAGACAATAGCAGGATGCTGGGGAGCTCTTCGCTTCTCGCTCAC	3146

QY	3901	TGACTCGCTCGCTCGGTCGTTGGCTGCGGAGCGGTATCAGTCACTCAAGCGGCT	3960
Db	3147	TGACTCGCTCGCTCGGTCGTTGGCTGCGGAGCGGTATCAGTCACTCAAGCGGCT	3206
QY	3961	AATACGGTTATCCACAGAATCAGGGGATAAACGAGGAAAGAAACATGTAGCAAAAGGCCA	4020
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QY	4021	GCAAAAGGCCAGAAACCGTAAAAAGCCGTTGCTGGCGTTTTTTCATAGGCTCGGCC	4080
Db	3267	GCAAAAGGCCAGAAACCGTAAAAAGCCGTTGCTGGCGTTTTTTCATAGGCTCGGCC	3326
QY	4081	CCCTGACGAGCATCACAAAATTCGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGACT	4140
Db	3327	CCCTGACGAGCATCACAAAATTCGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGACT	3386
QY	4141	ATAAAGATACCAAGCGGTTTTCCCTCGGAAAGCTCCCTCGTGGCTCTCTGTTCCGACCT	4200
Db	3387	ATAAAGATACCAAGCGGTTTTCCCTCGGAAAGCTCCCTCGTGGCTCTCTGTTCCGACCT	3446
QY	4201	GCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATG	4260
Db	3447	GCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATG	3506
QY	4261	CTCAGCTCTAGGTATCTCAGTTCGGGTAGGTGCTTCGCTCAAGCTGGGCTGTGCA	4320
Db	3507	CTCAGCTCTAGGTATCTCAGTTCGGGTAGGTGCTTCGCTCAAGCTGGGCTGTGCA	3566
QY	4321	CGAAACCCCGCTTACGCGCGACCGCTGCGCTTTATCCGGTAACTATCGTCTGAGTCCAA	4380
Db	3567	CGAAACCCCGCTTACGCGCGACCGCTGCGCTTTATCCGGTAACTATCGTCTGAGTCCAA	3626
QY	4381	CCCGTAAAGACACGACTTATTCGCACTGGCAGCAGCACCTGGTAAACAGGATAGCAGAGC	4440
Db	3627	CCCGTAAAGACACGACTTATTCGCACTGGCAGCAGCACCTGGTAAACAGGATAGCAGAGC	3686
QY	4441	GAGTATGTTAGGGGTGCTACAGAGTTCCTGAAGTGGTGGCTTAACTACGGCTACACTAG	4500
Db	3687	GAGTATGTTAGGGGTGCTACAGAGTTCCTGAAGTGGTGGCTTAACTACGGCTACACTAG	3746
QY	4501	AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTCGGAAAAAGAGTTGG	4560
Db	3747	AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTCGGAAAAAGAGTTGG	3806
QY	4561	TAGCTCTTGAATCCGGCAAAACAAACCAACCGCTGGTAGCGGTGGTTTTTTTGTGTCAGCA	4620
Db	3807	TAGCTCTTGAATCCGGCAAAACAAACCAACCGCTGGTAGCGGTGGTTTTTTTGTGTCAGCA	3866
QY	4621	GCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTTGTATCTTTTCTACGGGTC	4680
Db	3867	GCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTTGTATCTTTTCTACGGGTC	3926
QY	4681	TGACGCTCAGTGGAAACGAAAACTCAGTTAAGGGATTTTGGTCATGAGATTATCAAAAAG	4740
Db	3927	TGACGCTCAGTGGAAACGAAAACTCAGTTAAGGGATTTTGGTCATGAGATTATCAAAAAG	3986
QY	4741	GATCTTCACTAGATCTTTTAAATTAATAATGAAGTAAAAATCAATCTAAAGTATATA	4800
Db	3987	GATCTTCACTAGATCTTTTAAATTAATAATGAAGTAAAAATCAATCTAAAGTATATA	4046
QY	4801	TGAGTAAACCTTGGTCTGACAGTTTACCAATGCTTAAATCAGTGAGGCACTTATCTCAGGAT	4860
Db	4047	TGAGTAAACCTTGGTCTGACAGTTTACCAATGCTTAAATCAGTGAGGCACTTATCTCAGGAT	4106
QY	4861	CTGCTCTATTTCTGTTTCAATCCATAGTTGCTGACTCCCGCTGGTGTAGATACTACGATACG	4920
Db	4107	CTGCTCTATTTCTGTTTCAATCCATAGTTGCTGACTCCCGCTGGTGTAGATACTACGATACG	4166
QY	4921	GGAGGCTTACCAATCTGGCCCAAGTGTGCAATGATACCGCAGAGCCACGCTCACCGGC	4980
Db	4167	GGAGGCTTACCAATCTGGCCCAAGTGTGCAATGATACCGCAGAGCCACGCTCACCGGC	4226
QY	4981	TCCAGATTATCAGCAATAAACCAGCCAGCGGAGGCGGAGAGTGTGCTCTGC	5040

Db 4227 TCAGATTTATCAGCAATAAACAGCAGCGAGCGGCGGAGAGTGGTCTGC 4286
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 Db 4287 AACTTTATCCGCTCCATCAGTCTATTAACTGTCGCGGAGCTAGAGTAGTTC 4346
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 Db 4587 GCCATCCGTAAGATGCTTTCTGTGACTGCTGAGTACTCAACCAAGTCAATTTGAGAATA 4646
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 Db 4647 GTGTATGCGCGGACCGAGTGTCTTTCGCGCGGCTCAATACGGGAATACCGGCCACA 4706
 Qy 5461 TAGCAGAACTTTAAAAGTGTCTCATCTATGGAACGTTCTTCGGGCGGAAAACCTCTCAAG 5520
 Db 4707 TAGCAGAACTTTAAAAGTGTCTCATCTATGGAACGTTCTTCGGGCGGAAAACCTCTCAAG 4766
 Qy 5521 GATCTTACCGCTTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCCAACTGATCTTC 5580
 Db 4767 GATCTTACCGCTTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCCAACTGATCTTC 4826
 Qy 5581 AGCATCTTTTACTTTCACGAGCTTTCTGGGTGAGCAAAAACAGGAAGCAAAATCCCGC 5640
 Db 4827 AGCATCTTTTACTTTCACGAGCTTTCTGGGTGAGCAAAAACAGGAAGCAAAATCCCGC 4886
 Qy 5641 AAAAAAGGAATAAGCGGACACGGAATGTTGAATACTCATCTCTCTCTTTTCAATA 5700
 Db 4887 AAAAAAGGAATAAGCGGACACGGAATGTTGAATACTCATCTCTCTCTTTTCAATA 4946
 Qy 5701 TTATTGAAGCAATTTATCAGGTTTATTTGTTCTCATGAGCGGATACATATTTGAATGTATTTA 5760
 Db 4947 TTATTGAAGCAATTTATCAGGTTTATTTGTTCTCATGAGCGGATACATATTTGAATGTATTTA 5006
 Qy 5761 GAAAAATTAACAATAGGGGTTCCGCGCATATTTCCCGGAAAGTCCACCTGACGCTTA 5820
 Db 5007 GAAAAATTAACAATAGGGGTTCCGCGCATATTTCCCGGAAAGTCCACCTGACGCTTA 5066
 Qy 5821 AGAAACCATTTATCATGACATTAACCTATAAATAAGCGGTATCAGGAGGCGCTTTCG 5880
 Db 5067 AGAAACCATTTATCATGACATTAACCTATAAATAAGCGGTATCAGGAGGCGCTTTCG 5126
 Qy 5881 TC 5882
 Db 5127 TC 5128

RESULT 4

AAF83669
 ID AAF83669 standard; DNA; 6299 BP.

XX
 AC AAF83669;

XX
 DT 23-JUL-2001 (first entry)

XX
 DE HCV NS34A ORF comprising pCMV-NS34A nucleic acid sequence.

XX
 KW HCV; mutant; non-structural protein; NS; hepatitis C virus; mutation;
 KW catalytic domain; NS3; NS4; NS5; antiviral; vaccine; immunostimulant;
 KW immunotherapy; NS34A; ds.
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1990..4050
 FT /*tag= a
 FT /product= "NS34A"
 PN W0200138360-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000MO-US032326.
 PR 24-NOV-1999; 99US-0167502P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Coit D, Medina-Selby A, Selby M, Houghton M;
 XX WPI; 2001-343948/36.
 DR P-PSDB; AAB62633.
 XX
 PT Mutant non-structural (NS) Hepatitis C virus (HCV) polypeptide, useful as
 PT a vaccine against HCV, comprises a polypeptide having a mutation that
 PT functionally disrupts the catalytic domain of NS3.
 PS Disclosure; Fig 9; 340pp; English.
 XX
 CC The invention relates to an isolated mutant non-structural (NS) Hepatitis
 CC C virus (HCV) polypeptide, comprising a polypeptide having a mutation in
 CC the catalytic domain of NS3, where the mutation functionally disrupts the
 CC catalytic domain. The NS mutant polypeptides can include NS3, NS4 (NS4a
 CC and NS4b) NS5 (NS5a and NS5b) or portions thereof. The HCV polypeptide
 CC and polynucleotide (preferably DNA or a plasmid) compositions can be used
 CC in vaccines against HCV and as diagnostics. The antibodies raised against
 CC these polypeptides can also be used as diagnostics, or for passive
 CC immunotherapy. The antibodies are also useful for isolating and
 CC identifying HCV particles. The present sequence represents the nucleic
 CC acid sequence of the pCMV-NS34A comprising the ORF encoding a NS34A
 CC polypeptide
 XX
 SQ Sequence 6299 BP; 1449 A; 1713 C; 1637 G; 1500 T; 0 U; 0 Other;

Query Match 63.1%; Score 3713.6; DB 4; Length 6299;
 Best Local Similarity 77.4%; Pred. No. 0;
 Matches 4876; Conservative 0; Mismatches 1004; Indels 420; Gaps 14;

Qy 2 CGCGCGTTTCGGTGATGACGGTGAAGAAACCTCTGACACATGACGCTCCCGAGACGGTCA 61
 Db 1 CGCGCGTTTCGGTGATGACGGTGAAGAAACCTCTGACACATGACGCTCCCGAGACGGTCA 60
 Qy 62 AGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAGCCCGTCAGGCGCGCTCAGCGGGTGT 121
 Db 61 AGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAGCCCGTCAGGCGCGCTCAGCGGGTGT 120
 Qy 122 TGGCGGGTGTGCGGGCTGGCTTAACTATCGCGCATCAGAGCAGATGTTACTGAGAGTGCA 181
 Db 121 TGGCGGGTGTGCGGGCTGGCTTAACTATCGCGCATCAGAGCAGATGTTACTGAGAGTGCA 180
 Qy 182 CCATATGAAGCTTTTTCGAAAAAGCTAGGCTCCAAAAAGCTCTCTACTTCTCGGA 241
 Db 181 CCATATGAAGCTTTTTCGAAAAAGCTAGGCTCCAAAAAGCTCTCTACTTCTCGGA 240
 Qy 242 ATAGCTCAGAGCGCGGCGGCTCGGCTCTGTCATAAATAAAAAAATAGTCAGCCAT 301
 Db 241 ATAGCTCAGAGCGCGGCGGCTCGGCTCTGTCATAAATAAAAAAATAGTCAGCCAT 300

Db 2460 CGCGGTGTGCACCGTGGAGTGGCTAAGCGGTGGACTTTATCCCTGTGGAGAACCTAGA 2519
QY 2379 CACTACCCCCAAAACCTTGGCGT-----ATTGTCCCGCAGAGTGTGTGGT 2429
Db 2520 GACAAACATGAGTCCCGGTGTACGAGTAATCTCTCTCCACAGTAGTGCCTCCAGAG 2579
QY 2430 CCGGTATATGTCTCACTCCACCGCGGTGGTGGAGACGACCAAGGTCCGGCGG 2489
Db 2580 CTTCCAGGTGGCTCAGCTCATGTCCACAGGAGCGGCAAGACCAAGGTCCCGGC 2639
QY 2490 CCACCTACAGCTGGG-----TGAAATGATAGGA 2521
Db 2640 TGCATATGAGCTCAGGGCTAAGGTGCTAGTCAACCCCTCTGTGTCTCAACACT 2699
QY 2522 CGTCTTGTCTTAAACAATACCAAGGCCAGCGCTGGCAATGGTTCGGTGTGACCTGGAT 2581
Db 2700 GGGCTTGTGCTTACATGTCCAAGGCTATGAGTGCATCTTAACATCAGGACCGGGT 2759
QY 2582 GAATCAACT----- 2591
Db 2760 GAGAACAAATTACCACTGGCAGCGCCCATCAGTACTCCACCTACGGCAAGTTCTTCCGGA 2819
QY 2592 -----GGATTCACCAAGTGTGGAGGCG----- 2617
Db 2820 CGCGGGTGTCTCGGGGGCGCTTATGACATAAATTTGTGACGAGTGCCACTCCACGGA 2879
QY 2618 TCGTGTGTCTATCGAGGGGCGGGCAACACCCCTGCACTGCCCACTGATTTCTCG 2677
Db 2880 TGCACATCAATTTGGGCATTGGCACTGTCTTGGACAGAGACTCGGGGGGGAG 2939
QY 2678 CAAGCATCCGAGCGCACATCTCTCGGTGCGGTCCGGTCCCTGGATCACACCCAGGTG 2737
Db 2940 ACTGGTGTGCTGCCACCGCACCCCTCGGGCTCGTCACTGTGCCCATCCCAACAT 2999
QY 2738 CTGTGTGCACTACCGGTATAGGCTTTGGCATATCTTGTACCATCAACTACACATATT 2797
Db 3000 CGAGGAGTTGTCTGTGTCCAACCGAGAGATCCCTTTTACGGCAAGCTATCCCT 3059
QY 2798 TAAATCAGGATGTACGTGGGGGGTGCAGAACAGGC--TGAAGCTGCTGCAACTGG 2855
Db 3060 CGAAGTAATCAAGGGGGGAGACATCTCATCTTCTGTCTTCAAGAAAGTGGACGA 3119
QY 2856 ACBCGGGGCGAA--CGTTGGATCTGGAAGATAGGACAGGTCCGAGATCGATATGGAGA 2913
Db 3120 ACTCGCGCAAAAGCTGTGCAATTGGGCAATCAATGCCGTGGCTACTACCGGGTCTTGA 3179
QY 2914 ACATCATCAGGATTCCTAGGACCCCTGCTGCTGTTACAGCGGGGTTTTCTTGTGGA 2973
Db 3180 CGTGTCCGTCACTCCGACACGCGCGATGTTGTGCTGTGGCAACCGATGCCCTCATGAC 3239
QY 2974 CAAGAATCCTCAATACCGCAGAG-----TCTAGACTGCTGGTGGACTTCTCTC 3023
Db 3240 CGGCTATACCGGCACTTCCGACTCGGTGATAGACTGCAATACGTGTGTCAACCAGACGT 3299
QY 3024 AATTTTCTAGGGGATCTCCGCTGTGTCTTGGCCAAATTCGAGTCCCCAACTCCAAAT 3083
Db 3300 CGATTTCAGCTTGACCTTACCTTCACTTGAAGCAATCAACGCTCCCGCAAGTGTGT 3359
QY 3084 CACTACCAACCTCTGCTCCCAATTTGCTGCTGTTATCGCTGGATGTGCTCGGGCT 3143
Db 3360 CTCCCGCACTCAACGTCCGGGCGAGGACTGGCAGGGGGAAGCCAGGCATCTACAGATTGT 3419
QY 3144 TTATCATATCTCTCATCTGCTGCTATGCTCATCTTCTTATTTGTTCTTCTGGAT 3203
Db 3420 GGCACCGGGGAGGCGCCCTCCGGCATGTTCGACTCGTCCGTCTCTGTGAGTGTATGA 3479
QY 3204 TATCAAGGTATGTTTGGCCGTTTGTCTCTTAATTCAGGATCAACAAACAGTACGGGA 3263
Db 3480 CGCAGGCTGTGTTGATATGAGTCAACCGCCCGGAGACTACAGTTAGGCTACAGCGTA 3539
QY 3264 CCATGCAAAACCTGCAAGACTCTCTGTCTCAAGGCAACTCT----- 3302
Db 3540 CATGAACACCCCGGGCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGAGGGCGCTT 3599

QY 3303 ---ATGTTTCCCTCATGTTGCTGTACAAACCTACGATGGAATTCACCTGTATTCC 3359
Db 3600 TACAGSCCTCACTCATATAGATGCCACATTTCTATCCAGACAAAGCAGAGTGGGAGAA 3659
QY 3360 ATCCCATGCTCTCGGCTTTCCGAAATACCTATGGAAGTGGGCTCAGTTCGTTCTCT 3419
Db 3660 CTTCTCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGTAGGCTCAAGCCCCCTCCCC 3719
QY 3420 TGGCTCAGTTTACTAGTGCAATTTGTTAGTGTCTCGTAGGGCTTCCCCCACTGTTGG 3479
Db 3720 ATCGTGGGACAGATGTGGAAGTGTGTTGCTTGCCTCAAGCCACCTCATGCGGCAAC 3779
QY 3480 CTTTTCAGCTATATGGAATGATGTGATTTGGGGGCCAAAGTCTGTACAGCATCTGTAGTCCC 3539
Db 3780 ACCCTGCTATACAGACTGGCGCTGTTTCCAGAAATGAATCACCTTACGACCAACGCTAC 3839
QY 3540 TTTATAC----- 3547
Db 3840 CAAATACATCATGACATGATGTGCGCCGACCTGGAGGTCTGCACAGCACTTGGGTGCT 3899
QY 3548 ----- 3547
Db 3900 CGTTGGCGGCTCTGGCTGCTTTGGCCGCGTATTGCTGTCAAGAGGTGCGTGTGTCAT 3959
QY 3548 -----GCTGTACCAATTTTCTTCTCTGCTGTATACATTTTAAGAAATTCAGACTCGAG 3602
Db 3960 AGTGGGCGGCTGCTTCTGCTCGGGAAGCCGCAATCATACCTGACAGGAAGTCTCTTA 4019
QY 3603 CAAAGTCTGAAGAGCGCGCAAGATATCAAGGATCACTAGCGGTGTAGAGTCTCGTGATC 3662
Db 4020 CCGAGAGTTCGATGAGATGGAAGAGTGTAGGATCCACTACGCGTGTAGAGTCTCGTGATC 4079
QY 3663 AGCTCGACTGTCCTTCTAGTTGCCAGCATCTGTTGTCCTCCCTCCCGTGGCTTC 3722
Db 4080 AGCTCGACTGTCCTTCTAGTTGCCAGCATCTGTTGTTGCCCCCTCCCGTGGCTTC 4139
QY 3723 CTTGACCCCTGGAAGGTGCCACTCCCACTGCTCTTCTTAATAAATGAGAAATTCGATC 3782
Db 4140 CTTGACCCCTGGAAGGTGCCACTCCCACTGCTCTTCTTAATAAATGAGAAATTCGATC 4199
QY 3783 GAATGTCTGAGTAGTGTCTATTCTATTTCTGGGGGTGGGGTGGGCGAGAGCAAGGG 3842
Db 4200 GCATTGTCTGAGTAGTGTCTATTCTATTCTGGGGGTGGGGTGGGCGAGAGCAAGGG 4259
QY 3843 GAGGATTCGGGAAGCAATAGCAGCATCTGSGGAGCTTCCGCTTCTCGCTCACTG 3902
Db 4260 GAGGATTCGGGAAGCAATAGCAGCATCTGSGGAGCTTCTCCGCTTCTCGCTCACTG 4319
QY 3903 ACTCGCTCGCTCGGTCTGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTAA 3962
Db 4320 ACTCGCTCGCTCGGTCTGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTAA 4379
QY 3963 TACGTTATTCACAGAAATCAGGGGATAACGAGAAAGAAACATGTGAGCAAAAGGCGAGC 4022
Db 4380 TACGTTATTCACAGAAATCAGGGGATAACGAGAAAGAAACATGTGAGCAAAAGGCGAGC 4439
QY 4023 AAAAGCCAGGAACCGTAAAGGCGCGCTGCTGCGGTTTTCATAGGCTCCGCGCCC 4082
Db 4440 AAAAGCCAGGAACCGTAAAGGCGCGCTGCTGCGGTTTTCATAGGCTCCGCGCCC 4499
QY 4083 CTGACGAGCATCAAAAAATCGACGCTCAAGTCAAGGTGGGGAACCCGACAGGACTAT 4142
Db 4500 CTGACGAGCATCAAAAAATCGACGCTCAAGTCAAGGTGGGGAACCCGACAGGACTAT 4559
QY 4143 AAAGATACAGGGGTTTCCCTTGAAGCTCCCTCGTGGCTCTCTCTGTTCGACCGCTGC 4202
Db 4560 AAAGATACAGGGGTTTCCCTTGAAGCTCCCTCGTGGCTCTCTCTGTTCGACCGCTGC 4619
QY 4203 CGCTTACCGGATACCTGCTCGGCTTCTCCCTTGGGAGCGGTGGCGCTTCTCAATGCT 4262
Db 4620 CGCTTACCGGATACCTGCTCGGCTTCTCCCTTGGGAGCGGTGGCGCTTCTCAATGCT 4679

QY 4263 CACGCTGATAGGTATCTCAGTTCCGTTAGGTAGTTCGCTCCAGCTGGGCTGTGTGCACG 4322
DB |||||
QY 4680 CACGCTGATAGGTATCTCAGTTCCGTTAGGTAGTTCGCTCCAGCTGGGCTGTGTGCACG 4739
DB |||||
QY 4323 AACCCCGGTTACAGCCCGACCGCTCGGCTTATCCGTTAACTATCCGTTAGTTCACAAAC 4382
DB |||||
QY 4740 AACCCCGGTTACAGCCCGACCGCTCGGCTTATCCGTTAACTATCCGTTAGTTCACAAAC 4799
DB |||||
QY 4383 CGGTAAAGACACGATCTATCCCACTGCGCAGCAGCCACTGGTAACAGATTTAGCAGAGCGA 4442
DB |||||
QY 4800 CGGTAAAGACACGATCTATCCCACTGCGCAGCAGCCACTGGTAACAGATTTAGCAGAGCGA 4859
DB |||||
QY 4443 GGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGCTACACTAGAA 4502
DB |||||
QY 4860 GGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGCTACACTAGAA 4919
DB |||||
QY 4503 GGACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTTCGGAAAGAGTTGGTA 4562
DB |||||
QY 4920 GGACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTTCGGAAAGAGTTGGTA 4979
DB |||||
QY 4563 GCTCTTGATCCGGCAACAAACACACCGCTGGTATAGCGGTGTTTTTTTGGTGGTGAACGACG 4622
DB |||||
QY 4980 GCTCTTGATCCGGCAACAAACACACCGCTGGTATAGCGGTGTTTTTTTGGTGGTGAACGACG 5039
DB |||||
QY 4623 AGATTACGGCGCAGAAAAGAGTCTCAAGAGATCCTTTGATCTTTTACGGGCTCTG 4682
DB |||||
QY 5040 AGATTACGGCGCAGAAAAGAGTCTCAAGAGATCCTTTGATCTTTTACGGGCTCTG 5099
DB |||||
QY 4683 ACCTCAGTGGGAACGAAAACCTCAGCTTAAGGGATTTTGGTCAATGAGATATCAAAAAGGA 4742
DB |||||
QY 5100 ACCTCAGTGGGAACGAAAACCTCAGCTTAAGGGATTTTGGTCAATGAGATATCAAAAAGGA 5159
DB |||||
QY 4743 TCTTCACTAGATCTCTTTTAAATTAATAAATGAAGTTTTAAATCAATCTAAAGTATATAG 4802
DB |||||
QY 5160 TCTTCACTAGATCTCTTTTAAATTAATAAATGAAGTTTTAAATCAATCTAAAGTATATAG 5219
DB |||||
QY 4803 AGTAAACTGGTCTGACAGTTACCAATGCTTAATCAGTCAGGCACCTATCTCAGCGCATCT 4862
DB |||||
QY 5220 AGTAAACTGGTCTGACAGTTACCAATGCTTAATCAGTCAGGCACCTATCTCAGCGCATCT 5279
DB |||||
QY 4863 GTCTATTTCCGTTTCATCCATAGTTGCGCTGACTCCCGGTCGTTAGATAAATCAATACGATACGGG 4922
DB |||||
QY 5280 GTCTATTTCCGTTTCATCCATAGTTGCGCTGACTCCCGGTCGTTAGATAAATCAATACGATACGGG 5339
DB |||||
QY 4923 AGGGCTTACATCTGGCCCGCAGTGTGCAATATGATACCGGAGACCCACGCTACCGGCTC 4982
DB |||||
QY 5340 AGGGCTTACATCTGGCCCGCAGTGTGCAATATGATACCGGAGACCCACGCTACCGGCTC 5399
DB |||||
QY 4983 CAGATTTATCAGCAATAAACCCAGCCAGCCGAGGCGCAGAGCGCAGAGTGGTCTCTGCAA 5042
DB |||||
QY 5400 CAGATTTATCAGCAATAAACCCAGCCAGCCGAGGCGCAGAGCGCAGAGTGGTCTCTGCAA 5459
DB |||||
QY 5043 CTTTATCCGCTCCATCCAGTCTTAATTAATTTGTCGCGGAAGCTAGAGTAAGTTCGTCG 5102
DB |||||
QY 5460 CTTTATCCGCTCCATCCAGTCTTAATTAATTTGTCGCGGAAGCTAGAGTAAGTTCGTCG 5519
DB |||||
QY 5103 CAGTTAATAGTTTGGCAACAGTTGTCGCAATGCTACAGGCATCGTGGTGTCTACGCTCGT 5162
DB |||||
QY 5520 CAGTTAATAGTTTGGCAACAGTTGTCGCAATGCTACAGGCATCGTGGTGTCTACGCTCGT 5579
DB |||||
QY 5163 CGTTTCGGTATGGCTTCAATTCAGCTCCGGTTCCCAAGCATCAAGCGAGTTACATGATCCC 5222
DB |||||
QY 5580 CGTTTCGGTATGGCTTCAATTCAGCTCCGGTTCCCAAGCATCAAGCGAGTTACATGATCCC 5639
DB |||||
QY 5223 CCATGTTGTCAAAAAAGCGGTTAGTCTCTTCGGTCTCCGATCGTTGTGTCAGAAAGT 5282
DB |||||
QY 5640 CCATGTTGTCAAAAAAGCGGTTAGTCTCTTCGGTCTCCGATCGTTGTGTCAGAAAGT 5699
DB |||||
QY 5283 TGGCCGAGTGTATACATCATGGTTATGGCAGACTGCAATAATCTCTTACTGTGATGC 5342
DB |||||
QY 5700 TGGCCGAGTGTATACATCATGGTTATGGCAGACTGCAATAATCTCTTACTGTGATGC 5759
DB |||||
QY 5343 CATCCGTAAGATGCTTTTCTGTGACTGGTGAAGTACTCAACCAAGTCAATCTGAGAATAGT 5402

RESULT 5

AAD06790

ID AAD06790 standard; DNA; 4276 BP.

XX

AC AAD06790;

XX

DT 06-AUG-2001 (first entry)

XX

DE Plasmid pCMVII.

XX

KW Virus-like particle; immunogen; hepatitis B virus surface antigen; HBsAg;

KW HBV; chimeric antigen; hepatitis C virus; HCV; virucide; vaccine;

KW plasmid pCMVII; cyclic; circular; ds.

XX

OS Human cytomegalovirus.

OS

OS Homo sapiens.

OS

OS Bos sp.

OS

OS Unidentified.

OS

OS Chimeric.

XX

PN WO200138358-A2.

XX

PD 31-MAY-2001.

XX

PF 22-NOV-2000; 2000WO-US032249.

XX

PF 24-NOV-1999; 99US-0167224P.

XX

(CHIR) CHIRON CORP.

XX

PA Selby M, Glazer E, Houghton M;

XX

XX WPI; 2001-367661/38.

XX

PT Virus-like particle for use as an immunogen, comprising a first hepatitis

PT B virus surface antigen (HBsAg) and chimeric antigen comprising a second

PT HBsAg covalently linked to hepatitis C immunogenic polypeptide.

XX	Disclosure; Fig 1; 115pp; English.	
PS	The invention relates to a virus-like particle for use as an immunogen,	
CC	comprising a first hepatitis B virus surface antigen (HBsAg) and a	
CC	chimeric antigen comprising a second HBsAg which is covalently linked to	
CC	an hepatitis C virus (HCV) immunogenic polypeptide, where the first and	
CC	the second HBsAg each comprise a substantially complete S domain. The	
CC	virus-like particle is useful as immunogen and as vaccine. The present	
CC	sequence is plasmid pCMW11, a pUC19-based cloning vector designed for	
CC	expression in mammalian cells. It comprises human cytomegalovirus (CMV)	
CC	immediate early (IE) enhancer/promoter, human CMV intron A, a human	
CC	tissue plasminogen activator (tPA) leader, a bovine growth hormone poly A	
CC	terminator (tSgt), a ColEI origin of replication and an ampicillin	
CC	resistance (Amp R) gene. This plasmid is used for expression of HBsAg and	
CC	chimeric antigen for production of virus-like particle of the invention	
XX		
SQ	Sequence 4276 BP; 1043 A; 1086 C; 1067 G; 1080 T; 0 U; 0 Other;	
	Query Match 45.2%; Score 2658.4; DB 5; Length 4276;	
	Best Local Similarity 72.7%; Pred. No. 4.6e-276;	
	Matches 4275; Conservative 0; Mismatches 1; Indels 1606; Gaps 1;	
QY	1 TC GCGGTTTCGGTGATGACGGTGAACCTCTGACACATGCGAGCTCCGGAGCGGTCA 60	
DB		
QY	1 TC GCGGTTTCGGTGATGACGGTGAACCTCTGACACATGCGAGCTCCGGAGCGGTCA 60	
DB		
QY	61 CAGCTTGTCTGAAGCGGATGCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTG 120	
DB		
QY	61 CAGCTTGTCTGAAGCGGATGCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTG 120	
DB		
QY	121 TTGCGGGGTGTCGGGCTCGGCTTAACTATGCGGCTCAGAGCAGATTGTACTGAGAGTGC 180	
DB		
QY	121 TTGCGGGGTGTCGGGCTCGGCTTAACTATGCGGCTCAGAGCAGATTGTACTGAGAGTGC 180	
DB		
QY	181 ACCATATGAGCTTTTTCGAAAGCCTAGGCGCTCCAAAAGAGCCCTCCTCACTACTCTGG 240	
DB		
QY	181 ACCATATGAGCTTTTTCGAAAGCCTAGGCGCTCCAAAAGAGCCCTCCTCACTACTCTGG 240	
DB		
QY	241 AATAGCTCAGAGCCGAGCGGCTCGGCTCTGCTAATAATAAATAAATAATAGTCAGCCA 300	
DB		
QY	241 AATAGCTCAGAGCCGAGCGGCTCGGCTCTGCTAATAATAAATAAATAATAGTCAGCCA 300	
DB		
QY	301 TGGGCGGAGAAATGGGCGGAACTGGGCGGGAGGGAATTAATGGCTATTTGGCCATTTGCAT 360	
DB		
QY	301 TGGGCGGAGAAATGGGCGGAACTGGGCGGGAGGGAATTAATGGCTATTTGGCCATTTGCAT 360	
DB		
QY	361 AGTTGTATCTATATCATTAATATGTACATTTATTTGGCTCATGTCCTCAATATGACCGCCA 420	
DB		
QY	361 AGTTGTATCTATATCATTAATATGTACATTTATTTGGCTCATGTCCTCAATATGACCGCCA 420	
DB		
QY	421 TGTTCAGATTGATTAATGACTAGTTATTAATAGTAATCAATACGGGCTCAATTAGTTTCAT 480	
DB		
QY	421 TGTTCAGATTGATTAATGACTAGTTATTAATAGTAATCAATACGGGCTCAATTAGTTTCAT 480	
DB		
QY	481 AGCCCATATATGAGGTTCCGCGGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCG 540	
DB		
QY	481 AGCCCATATATGAGGTTCCGCGGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCG 540	
DB		
QY	541 CCCAAGACCCCGCCCATTTGACGTAATATGAGTATGTTTCCCATAGTAACCGCAATA 600	
DB		
QY	541 CCCAAGACCCCGCCCATTTGACGTAATATGAGTATGTTTCCCATAGTAACCGCAATA 600	
DB		
QY	601 GGGACCTTCCATGAGCTCAATGGGTGGAGTATTTACGGTAAATCGCCACTTGGCAGTA 660	
DB		
QY	601 GGGACCTTCCATGAGCTCAATGGGTGGAGTATTTACGGTAAATCGCCACTTGGCAGTA 660	
DB		
QY	661 CATCAAGTGTATCATATGCAAGTCCGCCCTTATTTGACGTCGTAATGAGCGTAAATGGCCC 720	
DB		
QY	661 CATCAAGTGTATCATATGCAAGTCCGCCCTTATTTGACGTCGTAATGAGCGTAAATGGCCC 720	
DB		
QY	721 GCTGGCATATGCCCAGTACATGACCTTACGGGACCTTTCCTACTTGGCAGTACATCTAC 780	
DB		

QY	1861	AGGCGAGTGTAGTCTGAGCAGTACTGTTGCTCGCGGGCGGCCACACAGACATAATAGCT	1920
DB	1861		
QY	1861	AGGCGAGTGTAGTCTGAGCAGTACTGTTGCTCGCGGGCGGCCACACAGACATAATAGCT	1920
DB	1861		
QY	1921	GACAGACTAACACAGTGTCTCTTTCCATGGGTCTTTCTGCACTACCGTCGACGAA	1980
DB	1921		
QY	1921	GACAGACTAACACAGTGTCTCTTTCCATGGGTCTTTCTGCACTACCGTCGAC---	1977
DB	1921		
QY	1981	TTCAAGCAATCATGGATGCAATGAAGAGAGGGCTGCTGTGTGCTGCTGTGTGGAG	2040
DB	1978	-----	1977
QY	2041	CAGTCTTGGTTTCCGCCAGCGCTAGCGAAACCCACGTACCGGGGAAAGTGCGGGCCACA	2100
DB	1978	-----	1977
QY	2101	CTGTGCTGGATTGTAGGCTCTCGCACCGGCCAAGCAGACAGTCCAGCTGATCA	2160
DB	1978	-----	1977
QY	2161	ACACCAACGCGAGTTGGCACTCAATAGCACGGCCCTGAACGTGAATGATGAGCTCAACA	2220
DB	1978	-----	1977
QY	2221	CGGCTGGTTGGCAGGCTTTTCTATCACCAAGTTCACTCTCAGGCTGTCCTGAGA	2280
DB	1978	-----	1977
QY	2281	GGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAAGGCTGGGGCCCTATCAGTTATG	2340
DB	1978	-----	1977
QY	2341	CCAAACGAGCGGCCCGCAACAGCGCCCTACTGTGCACTACCCGCCAAACCTTTGCG	2400
DB	1978	-----	1977
QY	2401	GTATTGTCCCGGAAGAGTGTGTGGTCCGGTATATTGTTCACTCCAGCCCCGTGG	2460
DB	1978	-----	1977
QY	2461	TGGTGGGAACGACCGACAGTCCGGCGGCCACCTACAGCTGGGGTGAAATGATACGG	2520
DB	1978	-----	1977
QY	2521	ACGTCTTGTCTTAAACAATACGAGCCACCGTGGCAATTGGTTTCGGTTGTACTGGA	2580
DB	1978	-----	1977
QY	2581	TGAACCTCACTGGATTACCAAAAGTGTGGAGGGCCCTCTTGTGTCATCGGAGGGCGG	2640
DB	1978	-----	1977
QY	2641	GCAACAACCTTGCACTGCCCACTGATTGCTTCCGCAAGCATCCGAGCCACATACT	2700
DB	1978	-----	1977
QY	2701	CTCGTGGCGCTCCGCTCCCTGGATCACACCAGGTGCTGTGCACTACCCGTATAGGC	2760
DB	1978	-----	1977
QY	2761	TTTGGCATTATCTTGTACCATCAACTACACCATATTTAAATCAGGATGTACGTGGAG	2820
DB	1978	-----	1977
QY	2821	GGGTGGAACACAGCTGGAAGCTCCCTGCAACTGGACCGGGGCGAAGCTTGGCATCGG	2880
DB	1978	-----	1977
QY	2881	AAGATAGGGACAGTCCGAGTCGATATGGAGAACATCATCAGGATTCCTAGGACCCC	2940
DB	1978	-----	1977

QY	2941	TGCTCGTGTACAGGGGGGTTTTTCTTGTTCACAAGATCTCTACAAATACCGCAGAGTC	3000
DB	1978	-----	1977
QY	3001	TAGACTCGTGTGGACTTCTCTCAATTTTCTAGGGGATCTCCCGTGTCTTGTGGCAAA	3060
DB	1978	-----	1977
QY	3061	ATTGCGAGTCCCAACCTCCAATCATCTACCAACCTCTGTCTCTCAATTTGTCTGGTT	3120
DB	1978	-----	1977
QY	3121	ATCGCTGGATGTCTGCGGCGTTTTTATCATATTCTCTTCATCTCTGCTATGCTCA	3180
DB	1978	-----	1977
QY	3181	TCTTCTTATTGGTCTTCTTGGATTATCAAGGTATGTGCGCGTTTGTCTCTAATTTCCAG	3240
DB	1978	-----	1977
QY	3241	GATCAACAACACCACTACGGGACCATGCAAAACCTGCAAGACTCTCTGTCAAGGCAACT	3300
DB	1978	-----	1977
QY	3301	CTATGTTCCCTCATGTGCTGTACAAACCTACGGATGGAATTTGCACCTGTATTTCCA	3360
DB	1978	-----	1977
QY	3361	TCCCATCGTCTGGGCTTTCGCAAAATACCTATGGAGTGGGCTCAGTCCGTTCTCTT	3420
DB	1978	-----	1977
QY	3421	GGCTCAGTTTACTAGTGCCATTTGTTCAGTGTTCGTAGGGCTTTCGCCCACTGTTTGGC	3480
DB	1978	-----	1977
QY	3481	TTTCAGCTATATGGATGATGTGTATTGGGGCCCAAGTCTGTACAGATCGTGAGTCCCT	3540
DB	1978	-----	1977
QY	3541	TTATACCGCTGTACCAATTTCTTTTGTCTCTGGGTATACATTTTAAAGAAATTCAGACTCG	3600
DB	1978	-----CTAAGAAATTCAGACTCG	1994
QY	3601	AGCAAGTCTAGAAAGCGCGCCAAAGATCAAGGATCCACTACGCTTAGAGCTCGCTGA	3660
DB	1995	AGCAAGTCTAGAAAGCGCGCCAAAGATCAAGGATCCACTACGCTTAGAGCTCGCTGA	2054
QY	3661	TCAGCTCAGCTGCTGCTTCTAGTTGCCAGCCATCTGTGTTTGGCCCTCCCGGTGCCT	3720
DB	2055	TCAGCTCAGCTGCTGCTTCTAGTTGCCAGCCATCTGTGTTTGGCCCTCCCGGTGCCT	2114
QY	3721	TCTTGACCTCGAAGGTGCCACTCCCACTGCTTTCTTAATAAATGAGGAAATTTGCA	3780
DB	2115	TCTTGACCTCGAAGGTGCCACTCCCACTGCTTTCTTAATAAATGAGGAAATTTGCA	2174
QY	3781	TGCAATGTCTGAGTAGTGTCTATTCTATTCTGGGGGTGGGGTGGGGAGGACAGCAAG	3840
DB	2175	TGCAATGTCTGAGTAGTGTCTATTCTATTCTGGGGGTGGGGTGGGGAGGACAGCAAG	2234
QY	3841	GGGGAGATTGGGAAGACAATAGCAGGCATGTGGGAGCTCTTCGCTTCTCGCTCAC	3900
DB	2235	GGGGAGATTGGGAAGACAATAGCAGGCATGTGGGAGCTCTTCGCTTCTCGCTCAC	2294
QY	3901	TGACTCGCTGCGCTCGGCTCGGCTGGGGAGCGGTATCAGTCTCACTCAAAAGCGGT	3960
DB	2295	TGACTCGCTGCGCTCGGCTCGGCTCGGCGAGCGGTATCAGTCTCACTCAAAAGCGGT	2354
QY	3961	AATACGGTTATCCACAGAATCAGGGGATTAACGAGGAAAGACATGTGAGCAAAAGCCA	4020
DB	2355	AATACGGTTATCCACAGAATCAGGGGATTAACGAGGAAAGACATGTGAGCAAAAGCCA	2414
QY	4021	GCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTTCATAGGCTCCGCC	4080

Db 2415 GCAAAAGCCAGGAACCGTAAAAAGGCGCGTGTGCTGGCGTGTTCATAGAGTCCGCCC 2474
QY 4081 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGGAAACCCGACAGACT 4140
Db 2475 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGGAAACCCGACAGACT 2534
QY 4141 ATAAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCCT 4200
Db 2535 ATAAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCCT 2594
QY 4201 GCGCTTACCGGATACCTGTCCGCTTTCCTTCCTGCGGAAGCGTGGCGCTTCTCAATG 4260
Db 2595 GCGCTTACCGGATACCTGTCCGCTTTCCTTCCTTCGGAAGCGTGGCGCTTCTCAATG 2654
QY 4261 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGTCTGCTCCAAAGCTGGGCTGTGTGCA 4320
Db 2655 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGTCTGCTCCAAAGCTGGGCTGTGTGCA 2714
QY 4321 CGAACCCCGCTTCAGCGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAA 4380
Db 2715 CGAACCCCGCTTCAGCGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAA 2774
QY 4381 CCCGGTAAGACACGACTTATCGGCATCTGGCAGCAGCACACTGGTAACAGGATTAAGCAGC 4440
Db 2775 CCCGGTAAGACACGACTTATCGGCATCTGGCAGCAGCACACTGGTAACAGGATTAAGCAGC 2834
QY 4441 GAGGTATGAGGCGGTCTACAGGTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAG 4500
Db 2835 GAGGTATGAGGCGGTCTACAGGTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAG 2894
QY 4501 AAGCACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGG 4560
Db 2895 AAGCACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGG 2954
QY 4561 TAGCTCTTGATTCGGGCAAAACAAACCCAGCTGTGTAGCGGTGGTGTGTTTGTGCAAGCA 4620
Db 2955 TAGCTCTTGATTCGGGCAAAACAAACCCAGCTGTGTAGCGGTGGTGTGTTTGTGCAAGCA 3014
QY 4621 GCAGATTACCGGCGAGAAAAGGATCTCAAGAGATCTTGCATGAGATTTATCAAAAAG 4680
Db 3015 GCAGATTACCGGCGAGAAAAGGATCTCAAGAGATCTTGCATGAGATTTATCAAAAAG 3074
QY 4681 TGACGCTCAGTGGAAAGAAAACCTCACGTTAAGGATTTTGGTATGAGATTTATCAAAAAG 4740
Db 3075 TGACGCTCAGTGGAAAGAAAACCTCACGTTAAGGATTTTGGTATGAGATTTATCAAAAAG 3134
QY 4741 GATCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATA 4800
Db 3135 GATCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATA 3194
QY 4801 TGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGAT 4860
Db 3195 TGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGAT 3254
QY 4861 CTGTCTATTTCTGTTTCATCCATAGTTGCTGACTCCCGCTCGTGTAGATACTACGATACG 4920
Db 3255 CTGTCTATTTCTGTTTCATCCATAGTTGCTGACTCCCGCTCGTGTAGATACTACGATACG 3314
QY 4921 GAGGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCCGAGACCCACGCTCACCGGC 4980
Db 3315 GAGGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCCGAGACCCACGCTCACCGGC 3374
QY 4981 TCCAGATTATCAGCANTAAACCCAGCCGAGGCGGAGGCGGAGAGTGGTCTGTC 5040
Db 3375 TCCAGATTATCAGCANTAAACCCAGCCGAGGCGGAGGCGGAGAGTGGTCTGTC 3434
QY 5041 AACTTTATCCGCTTCCATCCAGTCTATTAATTTGTCGGGAAGCTAGAGTAAGTAGTTTC 5100
Db 3435 AACTTTATCCGCTTCCATCCAGTCTATTAATTTGTCGGGAAGCTAGAGTAAGTAGTTTC 3494
QY 5101 GCCAGTTAATAGTTTGGCAACCGTGTGTCATTTGCTACAGGCATCGTGGTGTACGCGTC 5160

Db 3495 GCAGTTAATAGTTTCCGCAACGTTGTGCCATTTGTCTACAGGCATCGTGGTGTACGCTC 3554
QY 5161 GTCGTTTGTGTATGGCTTTCATTTAGCTCCCGTTCCTCAACGATCAAGCGGAGTTACATGATC 5220
Db 3555 GTCGTTTGTGTATGGCTTTCATTTAGCTCCCGTTCCTCAACGATCAAGCGGAGTTACATGATC 3614
QY 5221 CCCATGTTGTGCAAAAAAGCGGTAGCTCCTTTCGGTCTCCGATCGTTGTTCAGAAAGTAA 5280
Db 3615 CCCATGTTGTGCAAAAAAGCGGTAGCTCCTTTCGGTCTCCGATCGTTGTTCAGAAAGTAA 3674
QY 5281 GTTGGCCGAGTGTATCACTCATGTTATGGCAGCACTGCATATTTCTTTACTGTCTCAT 5340
Db 3675 GTTGGCCGAGTGTATCACTCATGTTATGGCAGCACTGCATATTTCTTTACTGTCTCAT 3734
QY 5341 GCCATCCGTAAGATGCTTTTCTGTGACTGTGTAGTACTCAACCAAGTCATTTCTGAGAATA 5400
Db 3735 GCCATCCGTAAGATGCTTTTCTGTGACTGTGTAGTACTCAACCAAGTCATTTCTGAGAATA 3794
QY 5401 GTGTATGCGGCGACCGAGTTGCTTTTCCCGCGCTCAATA CGGGATTAATACCGCGCACCA 5460
Db 3795 GTGTATGCGGCGACCGAGTTGCTTTTCCCGCGCTCAATA CGGGATTAATACCGCGCACCA 3854
QY 5461 TAGCAGAACTTTTAAAGTGTCTCATTTGGAACACGTTCTTTCGGGGGAAAACTCTCAAG 5520
Db 3855 TAGCAGAACTTTTAAAGTGTCTCATTTGGAACACGTTCTTTCGGGGGAAAACTCTCAAG 3914
QY 5521 GATCTTACCGCTGTTGAGATCCAGTTCCGATGTAACCCACTCTGTGCACCCCACTGATCTTC 5580
Db 3915 GATCTTACCGCTGTTGAGATCCAGTTCCGATGTAACCCACTCTGTGCACCCCACTGATCTTC 3974
QY 5581 AGCATCTTTTACTTTTCCACGAGCTTTCTGGGTGAGCAAAAAAGGAGGCAAAATGCCGC 5640
Db 3975 AGCATCTTTTACTTTTCCACGAGCTTTTCTGGGTGAGCAAAAAAGGAGGCAAAATGCCGC 4034
QY 5641 AAAAAAGGAATAAGGCGGACACGGAATGTTGAATACTCATACTCTTCTTTTTCATA 5700
Db 4035 AAAAAAGGAATAAGGCGGACACGGAATGTTGAATACTCATACTCTTCTTTTTCATA 4094
QY 5701 TTATTCAAGCATTTATCAGGTTTATTGTTCTCATGAGCGATACATATTTGAATGTTATTTA 5760
Db 4095 TTATTGAAGCATTTATCAGGTTTATTGTTCTCATGAGCGATACATATTTGAATGTTATTTA 4154
QY 5761 GAAAAATAAACAATAAGGGGTTCCGCGCACATTTCCCGAAAAAGTGCCACCTCAGCGCTA 5820
Db 4155 GAAAAATAAACAATAAGGGGTTCCGCGCACATTTCCCGAAAAAGTGCCACCTCAGCGCTA 4214
QY 5821 AGAAACCATTTATCATGACATTAACCTATAAAAAATAGCGGTATCAGGAGGCCCTTTTCG 5880
Db 4215 AGAAACCATTTATCATGACATTAACCTATAAAAAATAGCGGTATCAGGAGGCCCTTTTCG 4274
QY 5881 TC 5882
Db 4275 TC 4276

RESULT 6

AD104102
ID AD104102 standard; DNA; 10263 BP.

XX AD104102;

XX AC AC

XX 22-APR-2004 (first entry)

XX Vector pTnMod (CMV/Red).

XX ss; vector; transposase; promoter; insertion sequence; Kozak; Tn10;
KW ovalbumin; vitellogenin; polyA; conalbumin; enhancer; ovomucoid;
KW signal sequence; transgenic animal; Huntington's disease;
KW alpha-1-antitrypsin deficiency; Alzheimer's disease; breast cancer;
KW cystic fibrosis; galactosaemia; congenital hypothyroidism;
KW maple syrup urine disease; neurofibromatosis; phenylketonuria;
KW sickle cell disease; Smith-Lemli-Optiz Syndrome; autoimmune disease;
KW shipping fever; cattle; mastitis; bacterial; viral; infection; Types I;

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KW type; II; diabetes.
XX Synthetic.
XX Key Location/Qualifiers
XX misc_feature 1..130 a
FT /*tag= a
FT /note= "Remainder of F1(-) on from pBluescript11 sk(-)"
FT 131..132
FT /*tag= b
FT /note= "Residue from ligation of restriction enzyme sites
FT used in construction"
FT 133..1777
FT /*tag= c
FT /note= "CMV promoter/enhancer from pGwiz"
FT /note= "CMV promoter is modified by the addition of an
FT ACC sequence upstream of ATG"
FT 1778..1779
FT /*tag= d
FT /note= "Residue from ligation of restriction enzyme sites
FT used in construction"
FT 1780..2987
FT /*tag= e
FT /product= "Transposase"
FT /note= "Modified from Tn10 by optimising codons for
FT stability"
FT 2988..2993
FT /*tag= f
FT /note= "Two engineered stop codons"
FT 2994
FT /*tag= g
FT /note= "Residue from ligation of restriction enzyme sites
FT used in construction"
FT 2995..3410
FT /*tag= h
FT /note= "Taken from pGwiz"
FT 3415..3718
FT /*tag= i
FT /note= "Non-coding DNA residual from pNK2859"
FT 3719..3761
FT /*tag= j
FT /note= "Non-coding lambda DNA residual from pNK2859"
FT 3762..3831
FT /*tag= k
FT /note= "Left insertion sequence recognised by Tn10"
FT 3832..3837
FT /*tag= l
FT /note= "Residue from ligation of restriction enzyme sites
FT used in construction"
FT 3838..4044
FT /*tag= m
FT /note= "Multiple cloning site from pBluescript11 sk(-)"
FT /note= "May be used to insert the sequence of interest
FT into the vector"
FT 4049..5693
FT /*tag= n
FT /note= "CMV promoter/enhancer from pGwiz"
FT 5694..5701
FT /*tag= o
FT /note= "Residue from ligation of restriction enzyme sites
FT used in construction"
FT 5702..6617
FT /*tag= p
FT /note= "pRed reporter coding sequence including polyA
FT from pDsRed1.1"
FT 6618..7101
FT /*tag= q
FT /note= "Multiple cloning site from pBluescript11 sk(-)"
FT /note= "May be used to insert the sequence of interest
FT into the vector"
FT 7102..7106
FT /*tag= r
FT /note= "Residue from ligation of restriction enzyme sites

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FT insertion_seq used in construction"
FT 7107..7176
FT /*tag= s
FT /note= "Right insertion sequence recognised by Tn10"
FT 7177..7218
FT /*tag= t
FT /note= "Non-coding lambda DNA residual from pNK2859"
FT 7219..8062
FT /*tag= u
FT /note= "Non-coding DNA residual from pNK2859"
FT 8063..10263
FT /*tag= v
FT /note= "Remainder from pBluescript11 sk(-)"
XX
XX WO2004003157-A2.
XX
XX 08-JAN-2004.
XX
XX 26-JUN-2003; 2003WO-US020389.
XX
XX 26-JUN-2002; 2002US-0392415P.
XX 21-JAN-2003; 2003US-0441377P.
XX 21-JAN-2003; 2003US-0441381P.
XX 21-JAN-2003; 2003US-0441392P.
XX 21-JAN-2003; 2003US-0441405P.
XX 21-JAN-2003; 2003US-0441447P.
XX 21-JAN-2003; 2003US-0441502P.
XX
XX (TRAN-) TRANSGENRES LLC.
XX (LOUJ ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
XX Cooper RK, Cadd GG, Fioretti WC, Deboer KF;
XX WPI; 2004-083042/08.
XX
XX New vector comprising a transposase gene operably linked to a promoter,
XX useful in treating Alzheimer's disease, breast cancer, phenylketonuria,
XX autoimmune diseases, bacterial or viral infections or Types I and II
XX diabetes.
XX
XX Example 2; SEQ ID NO 2; 150pp; English.
XX
XX This sequence represents a new vector, pTnMod (CMV/Red), comprising a
XX transposase gene operably linked to a first promoter and one or more gene
XX of interest operably linked to one or more additional promoters, where
XX the one or more genes of interest and their operably linked promoters are
XX flanked by transposase insertion sequences recognized by the transposase
XX and the first promoter comprises a modified Kozak sequence comprising
XX ACCATG. The transposase is a Tn10 transposase and is modified in one to
XX twenty of the first codons. The gene of interest is operably linked to a
XX second promoter, which is a constitutive promoter or an inducible
XX promoter, e.g. an ovalbumin or a vitellogenin promoter. The vector
XX further comprises a polyA sequence, a conalbumin polyA sequence, operably
XX linked to the transposase gene. The vector further comprises two stop
XX codons operably linked to the transposase gene. The first or second gene
XX of interest is operably linked to a second or third promoter,
XX respectively. The first and a second gene of interest are operably linked
XX to a second promoter. The vector further comprises an enhancer operably
XX linked to the one or more genes of interest. The enhancer comprises at
XX least a portion of an ovalbumin enhancer. The vector further comprises an
XX egg directing sequence, ovalbumin or ovomucoid signal sequence or
XX vitellogenin targeting sequence, operably linked to the one or more genes
XX of interest. The vector is useful in producing transgenic animals with
XX desired proteins or molecules. They are also useful in treating
XX Huntington's disease, alpha-1-antitrypsin deficiency, Alzheimer's
XX disease, breast cancer, cystic fibrosis, galactosaemia, congenital
XX hypothyroidism, maple syrup urine disease, neurofibromatosis,
XX phenylketonuria, sickle cell disease, Smith-Lemli-Optiz Syndrome,
XX autoimmune diseases, shipping fever in cattle, mastitis, bacterial or
XX viral infections or Types I and II diabetes.
XX
XX Sequence 10263 BP; 2648 A; 2595 C; 2374 G; 2646 T; 0 U; 0 Other;

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Query Match		45.1%	Score 2654.4;	DB 12;	Length 10263;
Best Local Similarity		69.5%	Pred. No. 8.9e-276;		
Matches 4315;		Conservative	0;	Mismatches 1156;	Indels 737; Gaps 23;
QY	340	ATTGGCTATTGGCCATTCGATCGTTGCTATCTATATACATATAATATGATATATATGGC	399		
DB	4056	ATTGGCTATTGGCCATTCGATCGTTGCTATCCATATCATATAATATGATATATATGGC	4115		
QY	400	TCATGTCCAAATATGACCGCCATGTTGACATTTGATTTAGTACTAGTTATTAAATAGTAATCA	459		
DB	4116	TCATGTCCAAATATGACCGCCATGTTGACATTTGATTTAGTACTAGTTATTAAATAGTAATCA	4175		
QY	460	ATTACGGGGTCATTTAGTTTCATAGCCCATATATGAGAGTTCGCGTTACATAACTTACGGTA	519		
DB	4176	ATTACGGGGTCATTTAGTTTCATAGCCCATATATGAGAGTTCGCGTTACATAACTTACGGTA	4235		
QY	520	AATGGCCCGCTGGCTGACCGCCCAAGACCGCCCGCCCATTTGACGTCATATAAGTACGTAT	579		
DB	4236	AATGGCCCGCTGGCTGACCGCCCAAGACCGCCCGCCCATTTGACGTCATATAAGTACGTAT	4295		
QY	580	GTTCCCATAGTAACGCCAATAGGGACTTTTCCATTGACGTCATATGGGTGGAGTATTTACGG	639		
DB	4296	GTTCCCATAGTAACGCCAATAGGGACTTTTCCATTGACGTCATATGGGTGGAGTATTTACGG	4355		
QY	640	TAAACTGCCCATTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGAC	699		
DB	4356	TAAACTGCCCATTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGAC	4415		
QY	700	GTCAATGACGGTAATAGGCCCGCTGGCATATGCCAGTACATGACCTTTACGGGACTTT	759		
DB	4416	GTCAATGACGGTAATAGGCCCGCTGGCATATGCCAGTACATGACCTTTATGGGACTTTT	4475		
QY	760	CCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGTGATGCGGTTTGG	819		
DB	4476	CCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGTGATGCGGTTTGG	4535		
QY	820	CAGTACACCAATGGCGTGATAGCGTTTGTACTACCGGGATTTCCAAAGTCTCCACCCC	879		
DB	4536	CAGTACATCAATGGCGTGATAGCGTTTGTACTACCGGGATTTCCAAAGTCTCCACCCC	4595		
QY	880	ATTGACGTCAATGGGAGTTTGTGTGGCACCACCAATCAACGGGACTTTCCAAATGTGCT	939		
DB	4596	ATTGACGTCAATGGGAGTTTGTGTGGCACCACCAATCAACGGGACTTTCCAAATGTGCT	4655		
QY	940	AATAACCCCGCCCGTTGACGCAAAATGGCGGTAGCGGTGACGTTGCGGGAGGTCTATATA	999		
DB	4656	AACAATCCCGCCCGTTGACGCAAAATGGCGGTAGCGGTGACGTTGCGGGAGGTCTATATA	4715		
QY	1000	AGCAGAGCTCGTTTGTAGTGAACCGTCAAGTCGCTGGAGACGCCATCCACGCTGTTTGAC	1059		
DB	4716	AGCAGAGCTCGTTTGTAGTGAACCGTCAAGTCGCTGGAGACGCCATCCACGCTGTTTGAC	4775		
QY	1060	CTCATAGAAGACACCGGGACCGATCCAGCCTCGCGCCCGGGAAACGGTGCATTGGAACG	1119		
DB	4776	CTCATAGAAGACACCGGGACCGATCCAGCCTCGCGCCCGGGAAACGGTGCATTGGAACG	4835		
QY	1120	CGGATTTCCCGTCGCAAGAGTACGTTAAGTACCGCTATAGACTCTATAGGCACACCCCT	1179		
DB	4836	CGGATTTCCCGTCGCAAGAGTACGTTAAGTACCGCTCTATAGACTCTATAGGCACACCCCT	4895		
QY	1180	TTGGCTCTTATGCTACTACTGTTTGTGGCTTGGGGCTTATACACCCCGC-TCCTTA	1238		
DB	4896	TTGGCTCTTATGCTACTACTGTTTGTGGCTTGGGGCTTATACACCCCGCTTCTTAA	4955		
QY	1239	TGCTATAGGTGATGGTATAGCTTAGCCCTATAGTGTGGGTTATGACCATTTATGACCAC	1298		
DB	4956	TGCTATAGGTGATGGTATAGCTTAGCCCTATAGTGTGGGTTATGACCATTTATGACCAC	5015		
QY	1299	TCCCTCTATTGGTACCGATCTTTTCCATTAATATCAATACATGGCTCTTTTGGCACAAC	1358		
DB	5016	TCCCTCTATTGGTACCGATCTTTTCCATTAATATCAATACATGGCTCTTTTGGCACAAC	5075		
QY	1359	ATCTCTATTGGCTATATGCCAATACTCTGTCTTCTCAGAGACTGACACGGGACTCTGTATTT	1418		

DB	5076	ATCTCTATTGGCTATATGCCAATACTCTGTCTCCTCAGAGACTGACACGGACTCTGTATTT	5135		
QY	1419	TTACAGGATGGGGT-CCATTATTATTACAAATTCACATATACAAACAGCCGTCCTCCC	1477		
DB	5136	TTACAGGATGGGGTCCCAITTTATTATTACAAATTCACATATACAAACAGCCGTCCTCCC	5195		
QY	1478	GTGCCCCGAGTTTTTTATTAAACATAGCTGGGATCTCC--GACATCTCGGGTACGTGTT	1534		
DB	5196	GTGCCCCGAGTTTTTTATTAAACATAGCTGGGATCTCCACGCGAATCTCGGGTACGTGTT	5255		
QY	1535	CGGACATCGGCTCTTCTCCGTTAGCGCGGAGCTTCCACATCCGAGCCCTGTGTCATC	1594		
DB	5256	CGGACATCGGCTCTTCTCCGTTAGCGCGGAGCTTCCACATCCGAGCCCTGTGTCATC	5315		
QY	1595	CGTCCAGCGGCTCATGCTCGCTCGGAGCTCTTGTCTCTTAAACAGTGGAGGCCAGACTTA	1654		
DB	5316	CCTCCAGCGGCTCATGCTCGGAGCTCTTGTCTCTTAAACAGTGGAGGCCAGACTTA	5375		
QY	1655	GGCAGACACAATGCCACACACAGTGTGCGCACCAAGCCGTTGGCGGTAGGGTATG	1714		
DB	5376	GGCAGACACAATGCCACACACAGTGTGCGCACCAAGCCGTTGGCGGTAGGGTATG	5435		
QY	1715	TGTTCTGAAATGAGCTCGGAGATTGGGCTCGCAC-CTGGAACGAGATGGAAGACTTAAG	1773		
DB	5436	TGTTCTGAAATGAGCTCGGAGATTGGGCTCGCACCGCTCGACAGATGGAAGACTTAAG	5495		
QY	1774	CAGCGCACAAAGAGATGACGCGAGCTGAGTTGTGTGTTTCTGATTAAGAGTACAGAGTAA	1833		
DB	5496	CAGCGCACAAAGAGATGACGCGAGCTGAGTTGTGTGTTTCTGATTAAGAGTACAGAGTAA	5555		
QY	1834	CTCCCGTTCCGGTGTCTTAAACGGTGGAGGCGAGTGTAGTCTGACGAGTACTCGTTGCTG	1893		
DB	5556	CTCCCGTTCCGGTGTCTTAAACGGTGGAGGCGAGTGTAGTCTGACGAGTACTCGTTGCTG	5615		
QY	1894	CGCGCGCGCCACACAGACATAATAGCTGACAGACTAAACAGACTGTTCTTTCATGGGTC	1953		
DB	5616	CGCGCGCGCCACACAGACATAATAGCTGACAGACTAAACAGACTGTTCTTTCATGGGTC	5675		
QY	1954	TTTTCTGAGTCAACGCTCG-	1972		
DB	5676	TTTTCTGAGTCAACGCTCGCGCACAGGATCCACCGGTGCGCACCATCGTGGCTCTCTC	5735		
QY	1973	-----TCGACGAAATTCAGCAATCATGGATGCA-----	2000		
DB	5736	CAAGAACGTCAACAGGAGTTTCATCGCTTCAAGGTGCGCATGGAGGGCACCGTGAACGG	5795		
QY	2001	-----ATGAAGAGAGGGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2051		
DB	5796	CCACGAGTTTCGAGATTCGAGGCGAGGGCGAGGGCGCGCTTACGAGGGCCACCAACCCGT	5855		
QY	2052	TGCGCCAGCGCTAGCGAAACCCACGTCACCGGGGGAAGTCCCGGCCACACTGTGTCTGGA	2111		
DB	5856	GAAGCTGAAGGTGACCAAGGGCGGCCCTCTCGCTTTCGCGGACATCTCTGTCTCTCTCT	5915		
QY	2112	TTTGTGTAGCC-----	2121		
DB	5916	GTTCACAGTACGGCTCCAGGTGTACGTGAAGCACCCCGCGACATCCCGACTACAGAA	5975		
QY	2122	-----TCCTCGCACACAGGCGCCAAAGCAGAACGTCAGCTGTATCAACACACGGCAGTTG	2176		
DB	5976	GCTGTCTTCTCCCGAGGGCTTCAAGTGGAGGGCGGTGATGAATTCGAGGACCGCGCGT	6035		
QY	2177	GCACCTCAATAGCAGCGCCCTGNAATGCAATGATAGCTCAACACCGGCTGTGTGGCAGG	2236		
DB	6036	GGTGACGTGACCCAGGACTCTCTCCCTGCGAGGACGCTCTCTCATCTCAAGGTGAAGTT	6095		
QY	2237	GCTTTTCTATACCAACAGTCAACTCTTTCAGGCTCTCTGAGAGGCTAGCCAGCTGCCG	2296		
DB	6096	CATCGCGGTGAATTTCCCTCCGACGGCCCGCTTATGACAGAGAGAACCATGGCTGGGA	6155		
QY	2297	ACCCCTTACCGATTTTGACACAGGGCTGGGGCCCTATCATGTATGCAACGGAACGGGCC	2356		

Db 6156 GGCTCCACCGAGGGCTGTACCCCGCGAGCGGTGCTGAAGGCGAGATCCACAAGGC 6215
QY 2357 CGACGAGCGCCCTACTGCTGGCACTACC-----CCCCAA 2391
Db 6216 CTTGAAGCTGAAGGACGGCGCCACTACTGCTGGAGTTCAAGTCCATCTACATGGCCAA 6275
QY 2392 AACCTTGCCTATTGTGCCCGCAAGAGTGTGTGGTCCGGTATATTGCTTCACTCCC- 2450
Db 6276 GAAGCCGTCAGCTGCCCGGCTACTACTACGTTGGACTCCCAAGCTGGACATCACTCCCA 6335
QY 2451 -----AGCCCGTGGTGGGAACGACCGACAGGTGGGCGCGCCCACTACA 2499
Db 6336 CAACGAGGACTACACCATGTGAGCAGTACGAGCGCACCGAGGGCGCCACCCCTGTT 6395
QY 2500 GCTGGGTGAAAAATGA-----TACCGACGCTCTTCGT 2530
Db 6396 CCTGTAGCGCGCGACTCTAGATCATATAATCAGCCATACCACATTTGTAGAGGTTTACT 6455
QY 2531 CCTTAACAATACAGGCGCACCGCTGGCAATTGGTTGGTTGTACTGGATGACCTCAAC 2590
Db 6456 TGCTTTAAAAAACCTCCACACCTCCCCCTGAAACCTGAAACATAAAATGAATGCAATTGT 6515
QY 2591 TGGATTCAACAAAGTGTGGCGAGCGCTCCTGTGTATCGGAGGGCGGGCAACAACAC 2650
Db 6516 TGTGTAACTTGTATTGTCAGCTTATATGTTACAAATAAAGCAATAGCATCAAA 6575
QY 2651 CCT-----GCACTGCCCCCACTGATTC 2672
Db 6576 TTTCACAAATAAAGCATTTTTTTCATGCACTTCTAGTTGGGCCCGGCTGCAGGAATTC 6635
QY 2673 TTCGCGAAGCATCGGAGCGCACATCTCTCGGTGGGCTCCGGTCCCTGGATCACAACC 2732
Db 6636 GATATCAAGCTTATCGATACCGGTGACCTCGAGGGGGCGGCTACCCAAATTCGCCCTA 6695
QY 2733 AGTGTCTGTCTGACTACCG--TATAGGCTTTGGCATTATCTGTACCATCAATACA 2790
Db 6696 TAGTGAGTCGTATTACGGCGCTCATCTGGCCGTCTGTTTACAAGTCGTGACTGGGAATA 6755
QY 2791 CCATATTTAAAAATCAGGATGACGTGGAGGGTTCGAACACAGGCTGGAAGCTCCCTGCA 2850
Db 6756 CCCTGGGTTTACCAACTTAATCGCTTGCGACACATCCCTTTTCGCCAGCTGGCGTAA 6815
QY 2851 ACTGGACGGGGCGGACGTGGATCTGGAATAGGACAGCTTC-----2897
Db 6816 TAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTTGGCGAGCTGGAATGCGAATG 6875
QY 2898 GAGATCGATATGAGAACATCATACAGGATTCCTAGGACCCCTGCTCGTGTACAGGCG 2957
Db 6876 GAAATTTGAAGCGTTAATAATTTTGTAAATTCGGTTAAATTTTGTAAATCAGCTCA 6935
QY 2958 GGTTTTTCTTTGTGAAGAATCCTCACAATACCG-----2993
Db 6936 TTTTTTAACCAATAGGCGGAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACGAG 6995
QY 2994 -----CAGAGTCTAGACTCGTGGTGACTTCTCTC 3023
Db 6996 ATAGGTTGAGTGTGTTCAGTTTGGAAACAAGAGTCCACTATTAAGAAACGTGGACTCC 7055
QY 3024 AATTTTCTAGGGGATCTCCCGTGTGCTTGGCCA-----3058
Db 7056 AACGTCAAGGGCGAAAACCGTCTATCAGGGCGATGGCCCACTAATCCGGGATCATATG 7115
QY 3059 -----3058
Db 7116 ACAAGATGTGTATCCACCTTAATTAATGATTTTACCAAAATCAATTAGGGGATTCATCA 7175
QY 3059 -----3058
Db 7176 GTGCTCAGGCTCAACGGAATTAACAATTCGTCAGGAAGCTTATGATGATGATGTGCTT 7235
QY 3059 -----AAATTCGAGTCCCAACCTCCAATCACTCACCACCACTC 3097
Db 7236 AAAAACTTACTCAATGGCTGTTATGCATATCGCATATCGAATACATGCGAATAACCTTAAAGAGC 7295

QY 3098 CTGTCTCCOATTTGTCTCTGGTTATCGCTGGATGTGTCTCGGCGGTTT-----3145
Db 7296 TTGCGGATAAAAAAGGCCAAATTTATGTCTATTTACCGCGGCTTTTATTTAGCTGGAAG 7355
QY 3146 -----TATCATATTCCTCTTCATCTCTGCTGCTATGCTCATCTTCTT 3187
Db 7356 ATAAATAAAATAGATAGGTTTTTATTTGAAGCTAAATCTTCTTATCGTAAAAAATGCCCT 7415
QY 3188 ATTTGCTTCTCTGGATTATCAAGGTATGTTGCCCG-----3222
Db 7416 CTTGGGTATCAAGAGGTCATTATATTTTCGGGAATAACATCATTTTGGTGAAGAAATA 7475
QY 3223 -----3222
Db 7476 CTAAGCACTTGTCTCTCTTTACTCCCCCTGAGCTTGAGGGGTAAACATGAAGGTATCGA 7535
QY 3223 -----T 3223
Db 7536 TAGCAGGATAAATAACAGTAATAACGCTAAAACAATAATCCAAATCCAGGCATCCCAAT 7595
QY 3224 TTGTCTCTTAATTTCCAGGATCAACAACCAAGTACGGGACCATGCAAAACCTTGACGAC 3283
Db 7596 TGGTAGTGAATGATTATAATAACAGCAACAGTAATGGCCAAATAACCCGGTTGCAAT 7655
QY 3284 TCTGTCTCAAGGAACTCTATGTTTCCCTCATGTTGCTG-----3322
Db 7656 GGTAAAGGCTCAACCAATAATCCCTGTAAAGCACTTGTGATGACTCTTGTGTTGGATAGA 7715
QY 3323 -----TACAAAACCTACGGATGGAATTTGCACCTG 3352
Db 7716 CATCACTCCCTGATAATGACAGTAAGAGGATCCCAACACAGCCCAATAAATTTAAACAAG 7775
QY 3353 TATTCCTCATCCATCGCTCTGGGCTTTTCGCAAAATACCTATGGGAGTGGGCTCAGTCCG 3412
Db 7776 GAAACTTAACCAACCTTTCAGATATAAACGCTAAAAGGCAATGCACTACTATCTCAAT 7835
QY 3413 TTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTAGTGGTTCGTAGGGCTTTCCCCAC 3472
Db 7836 AAATCGAGCAGTACTGCGGCTTTTTCGCCCAATTTAGTGGCTATTCTCTGTCACAAAG 7895
QY 3473 TGTGTCCTTTTCAGCTATA-----TGGATCATGTGGTATTGGGGCCCAAG-----TCTGT 3522
Db 7896 GCTTGAATCTAGTGTAAAAGACCAAGACCGGTAATGAAAAGCCCAACCATCATGCTAT 7955
QY 3523 ACAGCATCGTAGTCCCTTTATACCGCTGTTTACCAATTTTCTTGTCTCTGGGTATACA 3582
Db 7956 TCATCATCAGATTTCTGTAAATAGCACACACCGTCTGGATTGGCTATCAATGCGCTGA 8015
QY 3583 TTTAAGAAATTCAGATCGAGCAAGTCTAGAAGGCGGCCAAGATATCAAGNATCCACTA 3642
Db 8016 AATAATAATCAACAAATGGCATCGTTAAATNAAGTATGATACCGGATCAGCTTTTGTTC 8075
QY 3643 CGGTTTAGAGCTCGCTGATCAGCTTCGAC-----TGTGCCCTTCTAGTTGCCAGCATC 3695
Db 8076 CTTTAGTAGGGTTAATTCGGCGCTTGGCGTAAATCATGGTCACTAGCTGTTTCTGTGTGA 8135
QY 3696 TGTGTTTTCCTCCCGCTGCTTCTTGTGACCCCTGGAAGGTGCCACTCCCACTGTCTCT 3755
Db 8136 AATTGTTATCCGCTCACAATTCACACAACATACAGCCGGAAGCATAAAGTGTAAAGCC 8195
QY 3756 TTCCTAATAAATAGAGAAATTCATCGCATTTGTCTGAGTAGTGTGTCATCTATTCTGGG 3815
Db 8196 TGGGTTGCCCTAATAGTAGTAACTCAATTAATTTGCGTTGCGCTCACTGCCCGCTTTC 8255
QY 3816 GGTGGGG-----TGGGCGAGACAGCAAGGGGAGGATTCGGAAGACAATAGACAGGATGC 3872
Db 8256 CAGTCGGGAACCTGTCTGTCAGCTGCAATTAATGAATCGGCCAACGCCGGGGAGAGGC 8315
QY 3873 -----TGGGAGCTCTTCCGCTTCTCGCTCACTGCTGCTCGGCTCGGTCGTT 3922
Db 8316 GGTTCGCTATTGGGCGCTCTTCGCTTCTCGCTCACTGACTGCTGCTGCGCTCGGTCGTT 8375

Qy	3923	CGGTCGGCGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCACAGAAATCA	3982
Dd	8376	CGGTCGGCGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCACAGAAATCA	8435
Qy	3983	GGGATAACCGAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACCGTAAA	4042
Dd	8436	GGGATAACCGAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACCGTAAA	8495
Qy	4043	AAGCCCGCTGTGCTGGCGTTTTCATAGGCTCGGCCCTCCCTGACAGCAATCAAAAAAT	4102
Dd	8496	AAGCCCGCTGTGCTGGCGTTTTCATAGGCTCGGCCCTCCCTGACAGCAATCAAAAAAT	8555
Qy	4103	CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGACTATAAGATACACAGGCTTTCC	4162
Dd	8556	CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGACTATAAGATACACAGGCTTTCC	8615
Qy	4163	CCTGGAGCTCCCTCGCTGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC	4222
Dd	8616	CCTGGAGCTCCCTCGCTGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC	8675
Qy	4223	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGT	4282
Dd	8676	GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGT	8735
Qy	4283	TCGGTGTAGGTCTGCTCCAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGAC	4342
Dd	8736	TCGGTGTAGGTCTGCTCCAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGAC	8795
Qy	4343	CGCTGGCCTTATCCGGTAACTATCGTTGAGTCCAAACCCGCTAAGACAGCTTATCG	4402
Dd	8796	CGCTGGCCTTATCCGGTAACTATCGTTGAGTCCAAACCCGCTAAGACAGCTTATCG	8855
Qy	4403	CCACTGGCAGCAGCACTGGTAACAGGATTAAGCAGAGCGAGGTATGTAGCGGTGTCTACA	4462
Dd	8856	CCACTGGCAGCAGCACTGGTAACAGGATTAAGCAGAGCGAGGTATGTAGCGGTGTCTACA	8915
Qy	4463	GAGTCTTTGAAGTGGTGGCTAACTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGC	4522
Dd	8916	GAGTCTTTGAAGTGGTGGCTAACTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGC	8975
Qy	4523	GCTCTGCTGAAGCAGTACCTTCGGAAAGAGTTGGTAGCTCTTGATCCGGCAACAA	4582
Dd	8976	GCTCTGCTGAAGCAGTACCTTCGGAAAGAGTTGGTAGCTCTTGATCCGGCAACAA	9035
Qy	4583	ACCACCGCTGTAAGCGGTGTTTTTTTGTGCAAGCAGCAGATTAAGCGCAGAAAAAA	4642
Dd	9036	ACCACCGCTGTAAGCGGTGTTTTTTTGTGCAAGCAGCAGATTAAGCGCAGAAAAAA	9095
Qy	4643	GGATCTCAAGAAGATCCTTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAC	4702
Dd	9096	GGATCTCAAGAAGATCCTTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAC	9155
Qy	4703	TCAGTTAAGGATTTTGGTCATGAGATTAATAAAGGATCTTACCTAGATCCTTTTA	4762
Dd	9156	TCAGTTAAGGATTTTGGTCATGAGATTAATAAAGGATCTTACCTAGATCCTTTTA	9215
Qy	4763	AATTAATAATGAAGTTTAAATCAATCTAAGTATATATCAGTAAACTTGGTCTGACAGT	4822
Dd	9216	AATTAATAATGAAGTTTAAATCAATCTAAGTATATATCAGTAAACTTGGTCTGACAGT	9275
Qy	4823	TACCAATGCTTAATCAGTAGGACCCCTATCTCAGCGATCTGTCTATTTTGGTTCATCCATA	4882
Dd	9276	TACCAATGCTTAATCAGTAGGACCCCTATCTCAGCGATCTGTCTATTTTGGTTCATCCATA	9335
Qy	4883	GTTGCTGACTCCCGCTGCTGTAGATTAATACGATACGGAGGCTTACCATCTGGCCCC	4942
Dd	9336	GTTGCTGACTCCCGCTGCTGTAGATTAATACGATACGGAGGCTTACCATCTGGCCCC	9395
Qy	4943	AGTGCTGCAATGATACCGCAGACCCGCTCAACCGCTCCAGATTTATCAGCAATAAAC	5002
Dd	9396	AGTGCTGCAATGATACCGCAGACCCGCTCAACCGCTCCAGATTTATCAGCAATAAAC	9455
Qy	5003	CAGCCAGCCGGAAGGGCCGAGCGCAGAGTGTCTCTGCACTTTATCCGCTCCATCCAG	5062

Dd	9456	CAGCCAGCCGGAAGGGCCGAGCGCAGAGTGTCTCTGCAACTTTATCCGCTCCATCCAG	9515
Qy	5063	TCCTATTAAATTTGTCGGGGAAGCTACAGTAAGTAGTTCGCCAGCTTAATAGTTTGGCGAAC	5122
Dd	9516	TCCTATTAAATTTGTCGGGGAAGCTACAGTAAGTAGTTCGCCAGCTTAATAGTTTGGCGAAC	9575
Qy	5123	GTTTGTGCCATTTGCTACAGGCATCGTGTGTCTACGCTCGTCTGTTGGTATGGCTTCATTC	5182
Dd	9576	GTTTGTGCCATTTGCTACAGGCATCGTGTGTCTACGCTCGTCTGTTGGTATGGCTTCATTC	9635
Qy	5183	AGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCGCCATGTTGTGCAAAAAAGCG	5242
Dd	9636	AGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCGCCATGTTGTGCAAAAAAGCG	9695
Qy	5243	GTTTAGCTCTCTCGGTCTCCGATCGTGTGTGTCAGAAAGTAAAGTTGGCCGAGTTATCACTC	5302
Dd	9696	GTTTAGCTCTCTCGGTCTCCGATCGTGTGTGTCAGAAAGTAAAGTTGGCCGAGTTATCACTC	9755
Qy	5303	ATGGTTATGGCAGCACTGCATAATTTCTTACTGTCTATGCCATCCGTAAGATGCTTTTCT	5362
Dd	9756	ATGGTTATGGCAGCACTGCATAATTTCTTACTGTCTATGCCATCCGTAAGATGCTTTTCT	9815
Qy	5363	GTGACTGTGTGAGTACTCAACCAAGTCAATCTCTGAGAAATAGTGTATGCGGCGACCGAGTTGC	5422
Dd	9816	GTGACTGTGTGAGTACTCAACCAAGTCAATCTCTGAGAAATAGTGTATGCGGCGACCGAGTTGC	9875
Qy	5423	TCCTGCGCCGGCTCAATACGGGATATACGGCCACATAGCAGAACTTTTAAAGTGCTC	5482
Dd	9876	TCCTGCGCCGGCTCAATACGGGATATACGGCCACATAGCAGAACTTTTAAAGTGCTC	9935
Qy	5483	ATCATTTGAAAAAGCTTTCTTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCC	5542
Dd	9936	ATCATTTGAAAAAGCTTTCTTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCC	9995
Qy	5543	AGTTCGATGTAAACCCACTCGTGCAACCACTGATCTTCAGCATCTTTTACTTTTACACGAC	5602
Dd	9996	AGTTCGATGTAAACCCACTCGTGCAACCACTGATCTTCAGCATCTTTTACTTTTACACGAC	10055
Qy	5603	GTTTCTCGGTGAGCAAAACAGGAGGCAAAATGCGCAAAAAGGGAATTAAGGGCGACA	5662
Dd	10056	GTTTCTCGGTGAGCAAAACAGGAGGCAAAATGCGCAAAAAGGGAATTAAGGGCGACA	10115
Qy	5663	CGAAATGTTGAATACTCATCTCTTCTCTTTTCAATATTTTGAAGCATTTATCAGGGT	5722
Dd	10116	CGAAATGTTGAATACTCATCTCTTCTCTTTTCAATATTTTGAAGCATTTATCAGGGT	10175
Qy	5723	TATTTGCTCATGAGCGGATACATATTTTGAATGTATTTAGAAAAATAAACAATAGGGTT	5782
Dd	10176	TATTTGCTCATGAGCGGATACATATTTTGAATGTATTTAGAAAAATAAACAATAGGGTT	10235
Qy	5783	CGCGCAGCATTTCCCGGAAAGTGCCAC	5810
Dd	10236	CGCGCAGCATTTCCCGGAAAGTGCCAC	10263

RESULT 7

AAF83668	standard; DNA; 4282 BP.
ID	AAF83668
XX	AAF83668;
AC	AC
XX	XX
DT	23-JUL-2001 (first entry)
XX	XX
DE	pCMV-II nucleic acid sequence.
XX	XX
KW	HCV; mutant; non-structural protein; NS; hepatitis C virus; mutation;
KW	catalytic domain; NS3; NS4; NS5; antiviral; vaccine; immunostimulant;
KW	immunotherapy; NS35; ds.
OS	Synthetic.
OS	Human cytomegalovirus.
OS	Bos sp.

XX	W0200138360-A2.	QY	481	AGCCCATATATGAGTTCCGCGTTACATAA	CTTACGGTAAATGGCCCGCTGCGTACCG	540
XX	31-MAY-2001.	DB	481	AGCCCATATATGAGTTCCGCGTTACATAA	CTTACGGTAAATGGCCCGCTGCGTACCG	540
XX	22-NOV-2000; 2000WO-US032326.	QY	541	CCCAACGACCCCGCCCAATTGACGTC	CAATAAATGACGTATGTTCCCATAGTAACGCAATA	600
XX	24-NOV-1999; 99US-0167502P.	DB	541	CCCAACGACCCCGCCCAATTGACGTC	CAATAAATGACGTATGTTCCCATAGTAACGCAATA	600
XX	(CHIR) CHIRON CORP.	QY	601	GGGACTTTCCATGACGTC	CAATGGGFGAGTATTTACGGTAAACTCCCACTTGGCAGTA	660
XX	Coit D, Medina-Selby A, Selby M, Houghton M;	DB	601	GGGACTTTCCATGACGTC	CAATGGGFGAGTATTTACGGTAAACTCCCACTTGGCAGTA	660
XX	WPI; 2001-343948/36.	QY	661	CATCAGTGTATCATATG	CCCAAGTCGCGCCCTATTGACGTCAATGACCGTAAATGGCCC	720
XX	Mutant non-structural (NS) Hepatitis C virus (HCV) polypeptide, useful as	DB	661	CATCAGTGTATCATATG	CCCAAGTCGCGCCCTATTGACGTCAATGACCGTAAATGGCCC	720
XX	a vaccine against HCV, comprises a polypeptide having a mutation that	QY	721	GCTGGCATTTAGCCCAAGTACATG	ACCTTTACGGGACTTTCCCTACTTTGGCAGTACATCTAC	780
XX	functionally disrupts the catalytic domain of NS3.	DB	721	GCTGGCATTTAGCCCAAGTACATG	ACCTTTACGGGACTTTCCCTACTTTGGCAGTACATCTAC	780
XX	Example 1; Fig 7; 340pp; English.	QY	781	GTATTAGTCAATCGCT	TAATACCATGCGTGTGGCAGGTACACCAATGGCGGTGA	840
XX	The invention relates to an isolated mutant non-structural (NS) Hepatitis	DB	781	GTATTAGTCAATCGCT	TAATACCATGCGTGTGGCAGGTACACCAATGGCGGTGA	840
XX	C virus (HCV) polypeptide, comprising a polypeptide having a mutation in	QY	841	TAGCGGTTTGACTC	ACGGGATTTCCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTG	900
XX	the catalytic domain of NS3, where the mutation functionally disrupts the	DB	841	TAGCGGTTTGACTC	ACGGGATTTCCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTG	900
XX	catalytic domain. The NS mutant polypeptides can include NS3, NS4 (NS4a	QY	901	TTTTGGCACCAAAATCAACGGGACTTTCCAA	AAATGTCGTAATAAACCCCGCTTTGACG	960
XX	and NS4b) NS5 (NS5a and NS5b) or portions thereof. The HCV polypeptide	DB	901	TTTTGGCACCAAAATCAACGGGACTTTCCAA	AAATGTCGTAATAAACCCCGCTTTGACG	960
XX	in vaccines against HCV and as diagnostics. The antibodies raised against	QY	961	CAATGGGCGGTAGGCGTGTACG	TGGGAGGTCTATATAAGCAGAGCTCGTTAGTAGAAC	1020
XX	the polypeptides can also be used as diagnostics, or for passive	DB	961	CAATGGGCGGTAGGCGTGTACG	TGGGAGGTCTATATAAGCAGAGCTCGTTAGTAGAAC	1020
XX	immunotherapy. The antibodies are also useful for isolating and	QY	1021	CGTCAGATCGCTGGAGAC	CCATCCACGCTGTTTTGACCTCCATAGACACACCCGGAC	1080
XX	identifying HCV particles. The present sequence represents the nucleic	DB	1021	CGTCAGATCGCTGGAGAC	CCATCCACGCTGTTTTGACCTCCATAGACACACCCGGAC	1080
XX	acid sequence of the pcMV-11 containing the human CMV promoter, enhancer,	QY	1081	CGATCCAGGCTCCGCGCGCGGAAACGGT	GTCATTTGGAACCGGATTTCCCGTGCACAGAGT	1140
XX	introns A, polylinker and the bovine growth hormone terminator in a	DB	1081	CGATCCAGGCTCCGCGCGCGGAAACGGT	GTCATTTGGAACCGGATTTCCCGTGCACAGAGT	1140
XX	deleted-pUC backbone	QY	1141	GAGTAAAGTACCGCTTATAG	CTCTATAGGCAACCCCTTTGGCTCTTATGCAATGCTATA	1200
XX	Sequence 4282 BP; 1044 A; 1089 C; 1068 G; 1081 T; 0 U; 0 Other;	DB	1141	GAGTAAAGTACCGCTTATAG	CTCTATAGGCAACCCCTTTGGCTCTTATGCAATGCTATA	1200
XX	Query Match 44.2%; Score 2601.2; DB 4; Length 4282;	QY	1201	CTGTTTTTGGCTTTGGGCGCTTAC	ACCCCGC-TCCCTATGCTATAGGTGATGCTATAGC	1259
XX	Best Local Similarity 72.5%; Pred. No. 5.8e-270;	DB	1201	CTGTTTTTGGCTTTGGGCGCTTAC	ACCCCGC-TCCCTATGCTATAGGTGATGCTATAGC	1259
XX	Matches 4268; Conservative 0; Mismatches 28; Indels 1612; Gaps 5;	QY	1260	TTAGCCCTATAGGTGTGGGTTATTG	ACCAATTTAGCCACTTCCCTATTGGTGCAGTACT	1319
XX	1 TCSCGCGTTTCGGTGATGACGGTGAAACCTCTGACACATGACAGTCCCGGACGCTCA	DB	1261	TTAGCCCTATAGGTGTGGGTTATTG	ACCAATTTAGCCACTTCCCTATTGGTGCAGTACT	1320
XX	60	QY	1320	TTCCATTAATACTAATCATATA	CAATGGCTCTTTGGCAACAATCTCTCTATTTGGCTATATGCCA	1379
XX	1 TCSCGCGTTTCGGTGATGACGGTGAAACCTCTGACACATGACAGTCCCGGACGCTCA	DB	1321	TTCCATTAATACTAATCATATA	CAATGGCTCTTTGGCAACAATCTCTCTATTTGGCTATATGCCA	1380
XX	60	QY	1380	ATACTCTGCTTTCAGAGACTGAC	CGGACTCTGTATTTTACAGATGGGT-CCATTT	1438
XX	61 CAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGCGCGTCAGCGGTG	DB	1381	ATACTCTGCTTTCAGAGACTGAC	CGGACTCTGTATTTTACAGATGGGTCCCATTT	1440
XX	120	QY	1439	ATTATTACAATAATTCATATA	CAACAACGCGCTCCCGCTGCCCGCAGTTTTTATTA	1498
XX	61 CAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGCGCGTCAGCGGTG	DB	1441	ATTATTACAATAATTCATATA	CAACAACGCGCTCCCGCTGCCCGCAGTTTTTATTA	1500
XX	120	QY	1499	CATAGCTGGGATCTCC	---GACATCTCGGTACGTTTCCGACATGGGCTCTTCCG	1555
XX	121 TTGGCGGCTTCGGGCTGCTTAACCTATGCGGCATCAGACAGATTTGTACTGAGAGTGC	DB	1501	CATAGCTGGGATCTCC	CGGAAATCTCGGTACGTTTCCGACATGGGCTCTTCCG	1560
XX	121 TTGGCGGCTTCGGGCTGCTTAACCTATGCGGCATCAGACAGATTTGTACTGAGAGTGC	QY	1556	GTAGCGGCGGAGCTTCCACAT	CCGAGCCCTGGTCCCATCGTCCAGCGGCTCATGTGTCG	1615

QY	3775	ATTGCATCGCATTTGTTCTGAGTAGGTGTCATTCTATTCTCGGGGGTGGGGTGGGCGAGGAC	3834
Db	2175	ATTGCATCGCATTTGTTCTGAGTAGGTGTCATTCTATTCTCGGGGGTGGGGTGGGCGAGGAC	2234
QY	3835	AGCAAGGGGAGGANTTGGGAAGAACAATAGCAGGCATGCTGGGAGCTCTTTCCGCTTCCCTC	3894
Db	2235	AGCAAGGGGAGGANTTGGGAAGAACAATAGCAGGCATGCTGGGAGCTCTTTCCGCTTCCCTC	2294
QY	3895	GCTCACTGACTCGCTGCGCTCGTTCGTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAA	3954
Db	2295	GCTCACTGACTCGCTGCGCTCGTTCGTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAA	2354
QY	3955	GGCGGTAAATACGGTTATCCACAAGTAACGGGTAACGCGAAGAAAGACATGTAGCAAA	4014
Db	2355	GGCGGTAAATACGGTTATCCACAAGTAACGGGTAACGCGAAGAAAGACATGTAGCAAA	2414
QY	4015	AGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCGGTTGCTGGCGTTTTTCCATAGGCT	4074
Db	2415	AGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCGGTTGCTGGCGTTTTTCCATAGGCT	2474
QY	4075	CCGCCGCCCTGA CGAGCATCACAAAAATCGA CGCTCAAGTCAGAGTGCGGAAACCCGAC	4134
Db	2475	CCGCCGCCCTGA CGAGCATCACAAAAATCGA CGCTCAAGTCAGAGTGCGGAAACCCGAC	2534
QY	4135	AGGACTATAAAGATACAGGCGTTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCC	4194
Db	2535	AGGACTATAAAGATACAGGCGTTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCC	2594
QY	4195	GACCTCGCCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGCGCTTTC	4254
Db	2595	GACCTCGCCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGCGCTTTC	2654
QY	4255	TCAATGCTCA CGCTGTAAGTATCTCAGTTCCGTTGTAAGTGGTTCGCTCCAAAGCTGGGCTG	4314
Db	2655	TCAATGCTCA CGCTGTAAGTATCTCAGTTCCGTTGTAAGTGGTTCGCTCCAAAGCTGGGCTG	2714
QY	4315	TGTGCAAGAACCCCGTTCAGCGCCGACCGCTCGGCTTATCCGTTAACTATCGTCTTGA	4374
Db	2715	TGTGCAAGAACCCCGTTCAGCGCCGACCGCTCGGCTTATCCGTTAACTATCGTCTTGA	2774
QY	4375	GTCCAAACCCGGTAAGACACAGACTTATCGCCACTGCGCAGCAGCCACTGGTAAACAGGATTAG	4434
Db	2775	GTCCAAACCCGGTAAGACACAGACTTATCGCCACTGCGCAGCAGCCACTGGTAAACAGGATTAG	2834
QY	4435	CAGAGCGAGGTA TGTAGGCGGTGCTA CAGAGTCTTGAAGTGGTGCGCTAACTA CCGGCTA	4494
Db	2835	CAGAGCGAGGTA TGTAGGCGGTGCTA CAGAGTCTTGAAGTGGTGCGCTAACTA CCGGCTA	2894
QY	4495	CACCTAGAACACAGTATTTGGTATCTGCGCTCTGCTGNAAGCCAGTTACCTTCGGNAAG	4554
Db	2895	CACCTAGAACACAGTATTTGGTATCTGCGCTCTGCTGNAAGCCAGTTACCTTCGGNAAG	2954
QY	4555	AGTTGGTAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTG	4614
Db	2955	AGTTGGTAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTG	3014
QY	4615	CAAGCAACAGATTA CCGCGCAGAAAAAAGGATCTCAAGAGATCCCTTTGATCTTTTCTAC	4674
Db	3015	CAAGCAACAGATTA CCGCGCAGAAAAAAGGATCTCAAGAGATCCCTTTGATCTTTTCTAC	3074
QY	4675	GGGGTCTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGGATTTTGGTCAATGAGATTATC	4734
Db	3075	GGGGTCTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGGATTTTGGTCAATGAGATTATC	3134
QY	4735	AAAAAGGATCTTCACTAGATCTTTTAAATAAAAATGAAGTTTTTAAATCAATCTAAAG	4794
Db	3135	AAAAAGGATCTTCACTAGATCTTTTAAATAAAAATGAAGTTTTTAAATCAATCTAAAG	3194
QY	4795	TATATATGATAAATCTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACTTATCTC	4854
Db	3195	TATATATGATAAATCTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACTTATCTC	3254

QY	4855	ACGATCTGCTCTATTCTGTTCAATCAATAGTTGCTGACTCCCGTCTGTTAGATAACTAC	4914
Db	3255	ACGATCTGCTCTATTCTGTTCAATCAATAGTTGCTGACTCCCGTCTGTTAGATAACTAC	3314
QY	4915	GATACGGGAGGGCTTACCACTCTGGCCCCAGTCTGCAATGATACCGCAGAGACCCAGCTC	4974
Db	3315	GATACGGGAGGGCTTACCACTCTGGCCCCAGTCTGCAATGATACCGCAGAGACCCAGCTC	3374
QY	4975	ACGGCTCCAGATTATCAGCAATAAACCCAGCCAGCGGGAAGGGCGAGGCAAGATGG	5034
Db	3375	ACGGCTCCAGATTATCAGCAATAAACCCAGCCAGCGGGAAGGGCGAGGCAAGATGG	3434
QY	5035	TCTCGCAACTTTATCCGCTCCATCCAGTCTATTAAATTGTTGCGGGAAGCTAGAGTAAAG	5094
Db	3435	TCTCGCAACTTTATCCGCTCCATCCAGTCTATTAAATTGTTGCGGGAAGCTAGAGTAAAG	3494
QY	5095	TAGTTCCGCAAGTTAATAGTTTCGCAACCGTTGTTGCTCATTTGCTACAGGCATCGTGTGTC	5154
Db	3495	TAGTTCCGCAAGTTAATAGTTTCGCAACCGTTGTTGCTCATTTGCTACAGGCATCGTGTGTC	3554
QY	5155	AGCTCGCTGTTGGTATGCTTCATTAGCTCCGTTCCCAACGATCAAGGCAAGTTAC	5214
Db	3555	AGCTCGCTGTTGGTATGCTTCATTAGCTCCGTTCCCAACGATCAAGGCAAGTTAC	3614
QY	5215	ATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCTTTCCGTTCTCCGATCGTGTGTCAG	5274
Db	3615	ATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCTTTCCGTTCTCCGATCGTGTGTCAG	3674
QY	5275	AAGTAAGTTGGCGCAGTGTATCACTCATGTTATGTCAGCAGCTGCATAAATCTCTTAC	5334
Db	3675	AAGTAAGTTGGCGCAGTGTATCACTCATGTTATGTCAGCAGCTGCATAAATCTCTTAC	3734
QY	5335	TGTCATGCCATCCGTAAGATGCTTTTCTGTGATGCTGAGTACTCAACCAAGTCAATTCG	5394
Db	3735	TGTCATGCCATCCGTAAGATGCTTTTCTGTGATGCTGAGTACTCAACCAAGTCAATTCG	3794
QY	5395	AGAAATAGTGTATGCGGCGACCGAGTTGCTCTTGGCCCGGCTCAATACGGGATAATAACCGC	5454
Db	3795	AGAAATAGTGTATGCGGCGACCGAGTTGCTCTTGGCCCGGCTCAATACGGGATAATAACCGC	3854
QY	5455	GCCACATAGCAGAACTTTTAAAAAGTCTCATTTGAAAAAGTCTTTCGGGGCGAAAACT	5514
Db	3855	GCCACATAGCAGAACTTTTAAAAAGTCTCATTTGAAAAAGTCTTTCGGGGCGAAAACT	3914
QY	5515	CTCAAGGATCTTACCGCTGTTGAGATCCAGTTGATTAACCACTCGTGCACCCCACTG	5574
Db	3915	CTCAAGGATCTTACCGCTGTTGAGATCCAGTTGATTAACCACTCGTGCACCCCACTG	3974
QY	5575	ATCTTCAGCATCTTTTACTTTTCAACAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAA	5634
Db	3975	ATCTTCAGCATCTTTTACTTTTCAACAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAA	4034
QY	5635	TGCGGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCTCTTTT	5694
Db	4035	TGCGGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCTCTTTT	4094
QY	5695	TCAATATATTGAAGCATTTTATCAGGGTTATTGTTCTCATGCGGATACATATTTGAATG	5754
Db	4095	TCAATATATTGAAGCATTTTATCAGGGTTATTGTTCTCATGCGGATACATATTTGAATG	4154
QY	5755	TATTTAGAAAAATAAAAAATAGGGGTTCCGGGCACATTTTCCCGAAAAAGTGCACCTGA	5814
Db	4155	TATTTAGAAAAATAAAAAATAGGGGTTCCGGGCACATTTTCCCGAAAAAGTGCACCTGA	4214
QY	5815	CGTCTAAGAAAAACATTTATCATGACATTAACCTATAAAAAATAGCGGTATCAACGAGGCC	5874
Db	4215	CGTCTAAGAAAAACATTTATCATGACATTAACCTATAAAAAATAGCGGTATCAACGAGGCC	4274
QY	5875	CTTTGCTC 5882	
Db	4275	CTTTGCTC 4282	

RESULT 8

ACCT71561
ID ACC71561 standard; DNA; 6236 BP.
XX
AC ACCT71561;
XX
DT 10-JUL-2003 (first entry)
XX
XX VRC6802(pVR1012x/s Lassa delta TW/h (codon optimised)) plasmid.
DE
DE Virucide; vaccine; immune response; Ebola virus; Marburg virus;
KW Lassa virus; retrovirus; paramyxovirus; influenza virus; adenovirus;
KW viral infection; filovirus; circular; cyclic; ds.
XX
OS Synthetic.
XX
XX W02003028632-A2.
PN
XX 10-APR-2003.
PD
XX 24-SEP-2002; 2002WO-US030251.
PF
XX 01-OCT-2001; 2001US-0326476P.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Nabel GJ, Yang Z, Sullivan N, Sanchez A;
PI
XX WPI; 2003-371961/35.
DR
XX
XX New bimodal priming and boosting compositions, useful as viral vaccines,
PT specifically for eliciting an immune response against a filovirus or a
PT disease caused by infection with filovirus.
XX
XX Claim 1; Page 211-213; 219pp; English.
PS
XX
CC The present invention relates to a bimodal priming composition and
CC boosting composition for priming and boosting an immune response to an
CC antigen in an individual. The compositions comprise (a) a priming
CC composition comprised of a DNA plasmid comprising a nucleic acid molecule
CC encoding Ebola, Marburg, Lassa, retrovirus, paramyxovirus or influenza
CC virus glycoprotein or nucleoprotein or their epitope-bearing domain, or a
CC DNA plasmid selected from ACC71521-ACC71563 and (b) a boosting
CC composition comprised of a replication-deficient adenovirus, comprising a
CC nucleic acid molecule encoding Ebola, Marburg, Lassa, retrovirus
CC paramyxovirus, or influenza virus glycoprotein or nucleoprotein or
CC epitope-bearing domain, or a replication deficient adenovirus selected
CC from constructs ACC71521-ACC71563. The compositions are useful as viral
CC vaccines, specifically for eliciting an immune response against a
CC filovirus or a disease caused by infection with filovirus e.g. Ebola
CC virus infection
XX
XX Sequence 6236 BP; 1574 A; 1658 C; 1559 G; 1445 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 2419.2; DB 10; Length 6236;
Best Local Similarity 70.9%; Pred. No. 1.4e-250;
Matches 3491; Conservative 0; Mismatches 1298; Indels 133; Gaps 16;
1 TC CGCGGCTTCGGTGATGACGGTGAACCTCTGACACATGCGAGCTCCCGGAGACGGTCA 60
1 TC CGCGGCTTCGGTGATGACGGTGAACCTCTGACACATGCGAGCTCCCGGAGACGGTCA 60
61 CAGCTTGCTGTGAAGCGGATGCGGGAGACAGACCGCTCAGGGCGGTCAAGCGGGTG 120
61 CAGCTTGCTGTGAAGCGGATGCGGGAGACAGACCGCTCAGGGCGGTCAAGCGGGTG 120
121 TTGGCGGGTGTCCGGGCTGCTTAACCTATATCGGGCATCAGACGAGATTGACTGAGAGTGC 180
121 TTGGCGGGTGTCCGGGCTGCTTAACCTATATCGGGCATCAGACGAGATTGACTGAGAGTGC 180
181 ACCATATGAAGCTTTTGGCAAAAGCCCTAGGCGCTCCAAAAGCCCTCTCTACTACTTCTGG 240
181 ACCATATGCGG-----TGTGAATAACCGCACA 207

QY 241 AATAGCTCAGAGCGGCGGCTCGGCTCTGTCATAATAAAAAAATTAGTCAGCCA 300
DB 208 GATGCGTAAGGAGAAATATACCGCATCAG----- 235
QY 301 TGGGCGGGAATGGCGGGAACCTGGCGGGGAGGGAATTATTGGCTATTGGCCATTGTCAT 360
DB 236 -----ATTGGCTATTGGCCATTGTCAT 256
QY 361 ACCTGCTATCTATCATATATGTACATTTATATTGGCTCATGTCCCAATATGACCGCCA 420
DB 257 ACCTGCTATCTATCATATATGTACATTTATATTGGCTCATGTCCCAATATGACCGCCA 316
QY 421 TGTGACATTTGATTATTGACTAGTTAATAGTAATCAATTACGGGGTCAATTAGTTTCAT 480
DB 317 TGTGACATTTGATTATTGACTAGTTAATAGTAATCAATTACGGGGTCAATTAGTTTCAT 376
QY 481 AGCCCATATATGAGTTCCGCGTTACATACTTACGGTAAATGGCGCGCTGCTGACCG 540
DB 377 AGCCCATATATGAGTTCCGCGTTACATACTTACGGTAAATGGCGCGCTGCTGACCG 436
QY 541 CCCAAGCAGCCCGCCCATTTGAGCTCAATAATGACGTATGTTCCCATAGTAAGCCCAATA 600
DB 437 CCCAAGCAGCCCGCCCATTTGAGCTCAATAATGACGTATGTTCCCATAGTAAGCCCAATA 496
QY 601 GGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAATGCCCCACTTTGGCAGTA 660
DB 497 GGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAATGCCCCACTTTGGCAGTA 556
QY 661 CATCAAGTGTATCATATGCAAGTCCGCGCTTATTTGACGTCAATGACGGTAAATGGCC 720
DB 557 CATCAAGTGTATCATATGCAAGTCCGCGCTTATTTGACGTCAATGACGGTAAATGGCC 616
QY 721 GCTGCGCATTTGCCCCAGTACATGACCTTACGGGACTTTCCCTACTTTGGCAGTACATCTAC 780
DB 617 GCTGCGCATTTGCCCCAGTACATGACCTTATGGGACTTTCCCTACTTTGGCAGTACATCTAC 676
QY 781 GTATTAGTTCATCGCTATTACCATGCTGCGGTTTGGCAGTACACCAATGGCGGTGA 840
DB 677 GTATTAGTTCATCGCTATTACCATGCTGCGGTTTGGCAGTACATCAATGGCGGTGA 736
QY 841 TAGCGGTTTGACTCAGCGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTG 900
DB 737 TAGCGGTTTGACTCAGCGGGATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTG 796
QY 901 TTTTGGCACCACCAATCAAACGGGACTTTCCAAATGTCGTAATACCCCGCCCGTTGACG 960
DB 797 TTTTGGCACCACCAATCAAACGGGACTTTCCAAATGTCGTAATACCCCGCCCGTTGACG 856
QY 961 CAAATGGCGGCTAGGGCTGTACGGTGGGAGTCTATATAAGCAGAGCTCGTTTAGTGAAC 1020
DB 857 CAAATGGCGGCTAGGGCTGTACGGTGGGAGTCTATATAAGCAGAGCTCGTTTAGTGAAC 916
QY 1021 CGTCAAGTCCGCTGGAGAGCCCATCCACGCTGTTTGGACTCCATAGAGACACCGGGAC 1080
DB 917 CGTCAAGTCCGCTGGAGAGCCCATCCACGCTGTTTGGACTCCATAGAGACACACCGGGAC 976
QY 1081 CGATCCAGCTCCGCGCGGGGACCGGTGCATTTGGAACCGGGATTCCTCGTGCACAGAT 1140
DB 977 CGATCCAGCTCCGCGCGGGGACCGGTGCATTTGGAACCGGGATTCCTCGTGCACAGAT 1036
QY 1141 GAGCTAAGTACCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCTATGCTATA 1200
DB 1037 GAGCTAAGTACCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCTATGCTATA 1096
QY 1201 CTGTTTTTGGCTTTGGGCTTATACACCCCGC--TCCTTATGCTATAGGTGATGGTATAGC 1259
DB 1097 CTGTTTTTGGCTTTGGGCTTATACACCCCGCTTCTTATGCTATAGGTGATGGTATAGC 1156
QY 1260 TTAGCCCTATAGGTGTTGGTATTGACCATTTGACCATTCCTCCCTATTTGGTACGATCT 1319
DB 1157 TTAGCCCTATAGGTGTTGGTATTGACCATTTTGGACCATTCCTCCCTATTTGGTACGATCT 1216

QY 1320 TTCCATTACTAATCCATAACATGGCTCTTTGCCACAACCTATCTCTATTGGCTATATGCCA 1379
DB 1217 TTCCATTACTAATCCATAACATGGCTCTTTGCCACAACCTATCTCTATTGGCTATATGCCA 1276
QY 1380 ATACTCTGTCTTTCAGAGCTGACACGGACTCTGTATTTTACAGAGTGGGT-CCATTTT 1438
DB 1277 ATACTCTGTCTTTCAGAGCTGACACGGACTCTGTATTTTACAGAGTGGGTCCCATTT 1336
QY 1439 ATTATTTACAAATTCATATACAAACAGCCGCTCCCGTCCCGCAGTTTTTTATAA 1498
DB 1337 ATTATTTACAAATTCATATATACAAACAGCCGCTCCCGCAGTTTTTTATAA 1396
QY 1499 CATAGCTGGGATCTCC---GACATCTCGGGTACGTGTTCCGACATGGCTCTTCTCG 1555
DB 1397 CATAGCTGGGATCTCCAGCGGAATCTCGGGTACGTGTTCCGACATGGCTCTTCTCG 1456
QY 1556 GTAGCGCGGAGCTTCCACATCCGAGCCCTGTGCTCCATCCGTCCAGCGCTCATGTGCG 1615
DB 1457 GTAGCGCGGAGCTTCCACATCCGAGCCCTGTGCTCCATCCGTCCAGCGCTCATGTGCG 1516
QY 1616 TCGGCACTCTCTTCTTAACAGTGGAGCCAGACTTAAGGCAAGCAATGCGGCCACCA 1675
DB 1517 TCGGCACTCTCTTCTTAAAGTGGAGCCAGACTTAAGGCAAGCAATGCGGCCACCA 1576
QY 1676 CACACAGTGTCCGCAACAGGCCCTGGCGTAGGGTATGTGCTGAAATGAGCTCGGAG 1735
DB 1577 CACACAGTGTCCGCAACAGGCCCTGGCGTAGGGTATGTGCTGAAATGAGCTCGGAG 1636
QY 1736 ATTTGGCTCGCAC-CTGGAGCGAGATGGAAGACTTAAGGCGAGCGGCAAGAGATGCGAG 1794
DB 1637 ATTTGGCTCGCACCGCTGACCGAGATGGAAGACTTAAGGCGAGCGGCAAGAGATGCGAG 1696
QY 1795 GCACTGAGTGTGTATTTCTGATAGAGTACAGAGTAACTCCGTTGCGGTGCTGTAA 1854
DB 1697 GCACTGAGTGTGTATTTCTGATAGAGTACAGAGTAACTCCGTTGCGGTGCTGTAA 1756
QY 1855 CGGTGAGGGCAGTGTAGTCTGAGAGTACTGTTGTCGCGCGCGGCAAGAGATGCGAG 1914
DB 1757 CGGTGAGGGCAGTGTAGTCTGAGAGTACTGTTGTCGCGCGCGGCAAGAGATGCGAG 1816
QY 1915 ATAGCTGACAGACTTAACAGACTGTTCTTTCAATGGTCTTTTCTGAGTACCGTCTC 1974
DB 1817 ATAGCTGACAGACTTAACAGACTGTTCTTTCAATGGTCTTTTCTGAGTACCGTCTC 1876
QY 1975 GACGAATTCAGCAATCATGGATG-CAATGAAGAGAGGGCTCTGCTGTGTGCTGCTG 2033
DB 1877 GACAGTGTGATCAGATATCGCGCGCTCTAGAGATATCGCGCCATGGCGCAGATCGT 1936
QY 2034 TGTGGAGCAGTCTTGTGTTGCGCCAGGCTAGCGAAACCCAG-TCACCGGGGAGTGC 2092
DB 1937 GACCTTTCTCCAGGAGGTGCCCATGTGATCGAGGAGGTGATGAACATCGTGTGATCGC 1996
QY 2093 CGGCCACACTGTCTGTGATTTGTATGACTCTCTCGCACAGGCGGCAAGCAGAACTGCA 2152
DB 1997 CTTGAGGCTGTGGCGTGTGAAGGCTGTACAACTTCGCCACTGTGGCCCTGTGGG 2056
QY 2153 GCTGATCAACACCAACCGCAGTTGGCACTCAATAGCAAGCGCCCTGAAGTCAATGATAG 2212
DB 2057 CTTGGTGAACCTTCTGTCTGTGCGGAGGAGCTGCACCAACAGCCTGTACAAAGGCGT 2116
QY 2213 CTTCAACACCGGCTGTGTGGCAGGCTTTCTATACCAAGATTCACTCTTCAGGCTG 2272
DB 2117 GTACGAGCTGCAGACCTTGAGCTGAACATGGAGACCTTGAAACATGACCAATGCCCTGAG 2176
QY 2273 TCTGAGAGGCTAGCAGCTGCGGACCCCTTACCGATTTTGGACAGGCTGTGGGCGCTAT 2332
DB 2177 CTGCAACAGAAACACAGCCACACTACATCATGTGTGGGCAACGACCGGCTGTGAGCT 2236
QY 2333 CAGTTATGCCAACGGAGCGGCCGCAACGAGCGCCCTACTCTGTGGCACTACCCCCAAA 2392
DB 2237 AACCTGACCAACACAGCATCATCAACCAAGATTCTGCAACCTGAGCGACGCCACAA 2296
QY 2393 ACCTTGGGTATTGTGCCCCG---GAAGAGTGTGTGCTCGGTATATTTGCTTCACTCC 2449

DB 2297 GAAGAACCTGTGACGACCGCCTGATGAGCATCATCAGACCTTCCACCTGAGCATCCC 2356
QY 2450 CAGCCCCGTGTGTGGGAAACGACGACAGGTCTGGGCGGCCACCTACAGCTGGGGTGA 2509
DB 2357 CAACTTCAACCACTAGAGGCGCATGAGCTGCGACTTCAACGGGGCAAGATCAGCGTGA 2416
QY 2510 AAATGATACGACGCTTCTGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 2569
DB 2417 GTACAACTGTGAGCCACAGCTAGCGCGGACGCGCAACCACTGCGGACCGTGGCCAA 2476
QY 2570 TTGTACTCTGATGAATCACTCACTGATTCACAAAGTGTGCGAGCGCTCTTGTCTCAT 2629
DB 2477 CGCGGTGTGACAGCTTTCATGAGGATGCGCTTGGGCGGACGCTACATCGCCTGACAG 2536
QY 2630 CCGAGGGGCGGGCAACAAACACCTGTCATGCCCCACTGATTTGCTTCCGAAGCATCCGA 2689
DB 2537 CGGAGGGGCAACTGGGACTGTCATGACACAGCTACAGTACCTGATCATCCAGAACAC 2596
QY 2690 CGGCCACATCTCTCGGTGCGGCTCCGTCCCTGATTCACACAGAGTGGCTGTGCTGACTA 2749
DB 2597 CACTGCGGAGGACCACTGCGAGTTTACGAGGCGCCAGCCCCATCGGCTACTTGGGCGCTGCT 2656
QY 2750 CCGGTATAGCTTTGSCATTTATCTTGTATCACTCACTCACTCACTCACTCACTCACT 2809
DB 2657 GAGCCAGAGAACGAGGACATCTACATCAGCAGAGGCTGTGGGCACTTCACTTGGAC 2716
QY 2810 GTACGTGGGAGGGGTGCAACACAGGCTGGAAGTGTGCTCACTGAGCGGGCGGAACG 2869
DB 2717 CTTGAGCGACGAGGCGCAAGACACACCGCGGCTACTGCTTACAGGTGGATGCT 2776
QY 2870 TTGCGATCTGGAAGATAGGACAGGTCCGAGATCGATATGAGAGAACATCACATCAGATT 2929
DB 2777 GATCGAGGCGGAGCTGAAGTGTCTCGGCAACACCGCGTGGCCAACTGCAACGAGAAGCA 2836
QY 2930 CTTAGGACCCCTGCTCGTGTACAGCGGGTCTTTCTTGTGCAAGAATCTCTCAAT 2989
DB 2837 CGACGAGGAGTCTGCGACATGCTGAGGCTGTGACCTTCAACAGCAGGCGCATCAGAG 2896
QY 2990 ACCGACAGTCTAGACTCGTGGTGGACTTCTCTCAATTTTCTAG-GGGGATCTCCGTTG 3048
DB 2897 GCTGAAGGCGGAGGCGCCAGATGAGCATCCAGCTGATCAACAGGCGGTGAACGCGCTGAT 2956
QY 3049 GTCTTGGCCAAATTTGCGAGTCCCAACTCAATCACTCACTCACTCTCTCTCTCTCCAA 3108
DB 2957 CAACGACAGCTGATCATGAAGAACCACTGTGAGGCACTCATGGGCACTCCCTACTGCAA 3016
QY 3109 TTTGTCTCTGTTATCGCTGGATGTCTCGGCG---GTTTATCATATTCTCTTCTCAT 3163
DB 3017 CTACAGCAAGTACTGTACTCTGAAACCAACCAACCGGAGGACGAGCTGCGCAAGTG 3076
QY 3164 CTTGCTGTCTATGCTCATCTTCTTATG-GTCTCTTGTGATTTATCAAGGTATGTTGCCG 3222
DB 3077 CTGGCTGTGTAGCAACGCGAGCTTACTGAAACGAGACCCACTTCAGCGACGACATCGAGCA 3136
QY 3223 TTTGTCTCTAATTCAGGATCAACAAACAGTACGAGCAACATGCAAACTCTGACGA 3282
DB 3137 GCAGGCGCAACATGATCACCGAGATGCTGCAAGAGGATACATGGAGGCGGCGCAA 3196
QY 3283 CTCCTCTCAAGCAACTCTATGTTTCC---CTCATGTTGTGTCACAAACCTTACGGATG 3339
DB 3197 GACCTGAAACGTTGGGATCAAGATCTGTGTCCTTCTAGTGGCCAGCATCTGTTGTTT 3256
QY 3340 GAAATGCACTGTATTTCCCATCCCATCGTCTGGGCTTTTCGCAAAATACCTATGGGAGT 3399
DB 3257 GCGCCTCCCGGCGCTCTCTTGACCTGGAAGGTGCCACTCCCACTGCTCTTCTCTAAT 3316
QY 3400 GGGCTCAGTCCGTTCTCTTGTGCTCAGTTTACTAGTGCATTTGTTGTTGTTGTTGTTG 3459
DB 3317 AAATGAGGAAATTTGATCGCATTTGTTGAGTAGGTGTCTATTTCTGGGGGGTGGG 3376
QY 3460 GGCTTCCCGCACTGTGTTGCTTTTCTGATATGAGTATGTTGTTGTTGTTGTTGTTG 3519

CC	determine the efficacy of the S gene segment of Seoul virus to provide
CC	protective immunity the gene segment was subcloned into the naked DNA
CC	expression vector pWRG7077 downstream of the cytomegalovirus immediate
CC	early promoter to yield pWRG/SEO-S. The construct was then used to
CC	challenge hamsters. Postchallenge serum samples from pWRG/SEO-S
CC	vaccinated hamsters were positive for glycoprotein and nucleocapsid
CC	antibodies
xx	
SQL	Sequence 6050 BP; 1634 A; 1416 C; 1454 G; 1546 T; 0 U; 0 Other;
	Query Match 40.8%; Score 2399.4; DB 3; Length 6050;
	Best Local Similarity 72.1%; Pred. No. 1.8e-248; Indels 240; Gaps 16;
	Matches 3457; Conservative 0; Mismatches 1096;
QY	337 ATTATTGGCTATTGGCCATTGCATACCTGTATCTATCATATAATATGTACATTATATT 396
DB	1263 AATATTGGCTATTGGCCATTGCATACCTGTATCTATCATATAATATGTACATTATATT 1322
QY	397 GGCTCATGTCCAATATGACGCCCATGTTCAGATTATTTGACTAGTTTAAATAGTAA 456
DB	1323 GGCTCATGTCCAATATGACGCCCATGTTCAGATTATTTGACTAGTTTAAATAGTAA 1382
QY	457 TCAATTACGGGTCAATTAGTTTCATAGCCCATATATGGAGTTTCGGCGTTACATACTTACG 516
DB	1383 TCAATTACGGGTCAATTAGTTTCATAGCCCATATATGGAGTTTCGGCGTTACATACTTACG 1442
QY	517 GTAATTGGCCCGCTGGCTGACGCCCCAAACGACCCCGCCCATTTGACGTCAATAATGACG 576
DB	1443 GTAATTGGCCCGCTCG-TGACCGCCCAACGACCCCGCCCATTTGACGTCAATAATGACG 1501
QY	577 TATGTTCCCATAGTAACGCCCAATAGGACATTTCCATTTGACGTCAATGGGTGGAGTATTTA 636
DB	1502 TATGTTCCCATAGTAACGCCCAATAGGACATTTCCATTTGACGTCAATGGGTGGAGTATTTA 1561
QY	637 CGGTAAACTGCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTAT 695
DB	1562 CGGTAAACTGCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGGCGCCCCCTAT 1621
QY	696 TGACGTCAATGACGGTAAATGGCCCGCTCGCATTTATGCCAGTACATGACCTTACGGGA 755
DB	1622 TGACGTCAATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTACATGACCTTACGGGA 1681
QY	756 CTTTCTACTTGGCAGTACATCTACGTTAGTGCATCGCTATTACCATGGTGATGCGGTT 815
DB	1682 CTTTCTACTTGGCAGTACATCTACGTTAGTGCATCGCTATTACCATGGTGATGCGGTT 1741
QY	816 TTGSCAGTACACCAATGGGCGTGATAGCGGTTTGACTCAGCGGGATTTCCAGTCTCCA 875
DB	1742 TTGSCAGTACACCAATGGGCGTGATAGCGGTTTTGACTCAGCGGGATTTTCCAGTCTCCA 1801
QY	876 CCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACCTTTCCAAAATG 935
DB	1802 CCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACCTTTCCAAAATG 1861
QY	936 TCGTAAATAACCCCGCCCGTTTGACGCAAAATGGGCGGTAGGCGGTGACGGTGGGAGGTCTA 995
DB	1862 TCGTAAATAACCCCGCCCGTTTGACGCAAAATGGGCGGTAGGCGGTGACGGTGGGAGGTCTA 1921
QY	996 TATAAGCAGAGCTCGTTTAGTGAACCGTTCAGATCGCTTCGAGACGCCATCCACGCTGTTT 1055
DB	1922 TATAAGCAGAGCTCGTTTAGTGAACCGTTCAGATCGCTTCGAGACGCCATCCACGCTGTTT 1981
QY	1056 TGACCTCCATAGAGACACCGGGACCGATCCAGCTCCCGGGCCGGGAAACGGTGCATTGG 1115
DB	1982 TGACCTCCATAGAGACACCGGGACCGATCCAGCTCCCGGGCCGGGAAACGGTGCATTGG 2041
QY	1116 AACCGGAGTTTCCCGGTGCCAAGAGTGCAGTAAAGTACCGCCCTATAGACTCTATAGGCAAC 1175
DB	2042 AACCGGAGTTTCCCGGTGCCAAGAGTGCAGTAAAGTACCGCCCTATAGACTCTATAGGCAAC 2101
QY	1176 CCCTTTGGCTCTTATGATGCTACTACTGTTTTTGGCTTTGGGGCCCTATACACCCCGCTCC 1235
DB	2102 CCCTTTGGCTCTTATGATGCTACTACTGTTTTTGGCTTTGGGGCCCTATACACCCCGCTCC 2161

Db 5398 GCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGTCTCGCT 5457
QY 4302 CCAAGCTGGCTGTGTGCAGAACCCCGCTTACGCCGCGCTGCGCTTATCCGGTA 4361
Db 5458 CCAAGCTGGCTGTGTGCAGAACCCCGCTTACGCCGCGCTGCGCTTATCCGGTA 5517
QY 4362 ACTATCGTCTTGTAGTCAACCCCGGTAGACACGACTTATCGCACCTGGCGAGCCACTG 4421
Db 5518 ACTATCGTCTTGTAGTCAACCCCGGTAGACACGACTTATCGCACCTGGCGAGCCACTG 5577
QY 4422 GTAAACAGGATTACAGACGAGGTATCTAGCGGTGCTACAGAGTCTTGAAGTGTGGC 4481
Db 5578 GTAAACAGGATTACAGACGAGGTATCTAGCGGTGCTACAGAGTCTTGAAGTGTGGC 5637
QY 4482 CTAACCTACGGCTACCTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAAGCCAGTTA 4541
Db 5638 CTAACCTACGGCTACCTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAAGCCAGTTA 5697
QY 4542 CCTTCGGAAGAGTGTGTAGCTCTTGATCCGGCAACAAACACCGCTGTAGCGGTG 4601
Db 5698 CCTTCGGAAGAGTGTGTAGCTCTTGATCCGGCAACAAACACCGCTGTAGCGGTG 5757
QY 4602 GTTTTTTTTTCAGACGACGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTT 4661
Db 5758 GTTTTTTTTTCAGACGACGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTT 5817
QY 4662 TGATCTTTTTCACGGGTCTGACGCTCAGTGGAAACCACTCACGTTAAGGATTTTGG 4721
Db 5818 TGATCTTTTTCACGGGTCTGACGCTCAGTGGAAACCACTCACGTTAAGGATTTTGG 5877
QY 4722 TCATGAGATTATCAAAAAGGATCTTACCTAGATCTCTTTTAAATTTAAATGAAGTTTA 4781
Db 5878 TCATGAGATTATCAAAAAGGATCTTACCTAGATCTCTTTTAAATTTAAATGAAGTTTA 5937
QY 4782 AATCAATCTAAAGTATATATGAGTAAACTTGTCTGACAGTTACCAATGCTTAATCAGTG 4841
Db 5938 AATCAATCTAAAGTATATATGAGTAAACTTGTCTGACAGTTACCAATGCTTAATCAGTG 5997
QY 4842 AGGCACCTATCTCAGCGATCTGTCTATTTGCTTCATCCATAGTTGCTGACTC 4894
Db 5998 AGGCACCTATCTCAGCGATCTGTCTATTTGCTTCATCCATAGTTGCTGACTC 6050

RESULT 10
ADK15555
ID ADK15555 standard; DNA; 6050 BP.
XX AC ADK15555;
XX AC ADK15555;
XX 03-JUN-2004 (first entry)
XX Seoul hantavirus S segment derived DNA vaccine pWRG/SEO-S.
DE virucide; gene therapy; hantavirus; M segment; L segment; S segment;
KW hantavirus infection; immune response; vaccine; hantavirus; seoul virus;
KW SEOV; DNA vaccine; SEOV S genomic segment; plasmid; cyclic; circular; ds;
KW pWRG/SEO-S.
XX Seoul virus.
OS Synthetic.
OS Synthetic.
XX US2004053216-A1.
FN 18-MAR-2004.
XX 21-MAR-2003; 2003US-00394388.
XX 29-AUG-2001; 2001US-00941974.
PR 22-MAR-2002; 2002US-0367128P.
PR 26-JUL-2002; 2002US-0398985P.
XX (HOOP/) HOOPER J W.
PA (SCHM/) SCHMALJOHN C S.

PA (CUST/) CUSTER M.
XX Hooper JW, Schmaljohn CS, Custer M;
PI WPI; 2004-247721/23.
XX New nucleic acid molecules and polypeptides useful for diagnosing,
PT preventing and treating hantavirus (e.g. hemorrhagic fever with renal
PT syndrome and/or hantavirus pulmonary syndrome hantavirus) infection.
XX Example 1; SEQ ID NO 4; 96pp; English.
XX The invention describes a nucleic acid (I), or its fragment, comprising a
CC fully defined sequence of 24 base pairs, as given in the specification.
CC Also described are: a recombinant DNA construct comprising a vector, at
CC least one hantavirus M gene nucleic acid fragment and the nucleic acid
CC fragment (I); a composition (II) comprising inert particles and a nucleic
CC acid coated onto the inert particles producing nucleic acid coated
CC particles, the nucleic acid comprising a promoter operative in the cells
CC of a mammal and a hantavirus polynucleotide M segment encoding G1 and G2
CC from one or more hantavirus; a therapeutic composition for ameliorating
CC symptoms of hantavirus infection, comprising the composition (II) and a
CC pharmaceutical excipient; inducing a protective immune response against
CC hantavirus infection in a mammal; a vaccine against infection with the
CC hantavirus, the vaccine comprising the composition (II); treating or
CC detecting hantavirus infection; and a hantavirus infection diagnostic kit
CC comprising the composition (II) and ancillary reagents for detecting the
CC presence or absence of hantavirus antigens in a sample. The composition
CC and methods are useful for diagnosing, preventing and treating hantavirus
CC infection. This sequence represents a SEOV hantavirus DNA vaccine
CC comprising the SEOV S (small) genomic segment.
XX SQ Sequence 6050 BP; 1634 A; 1417 C; 1453 G; 1546 T; 0 U; 0 Other;
Query Match 40.8%; Score 2397.8; DB 12; Length 6050;
Best Local Similarity 72.1%; Pred. No. 2.7e-248;
Matches 3456; Conservative 0; Mismatches 1097; Indels 240; Gaps 16;
QY 337 ATTATTTGGCTATTGGCCATTGTCATAGTGTATCTATATATATATATATATATAT 396
Db 1263 AATATTTGGCTATTGGCCATTGTCATAGTGTATCTATATATATATATATATAT 1322
QY 397 GGCTCATGTCCCAATATGACGCCCATGTTGACATTCGATTATTTAGTATTAAATAGTAA 456
Db 1323 GGCTCATGTCCCAATATGACGCCCATGTTGACATTCGATTATTTAGTATTAAATAGTAA 1382
QY 457 TCAATTTACGGGGTTCATTAGTTTCATAGCCCATATATGAGGTTCCGCGTTACATACTTACG 516
Db 1383 TCATTTACGGGGTTCATTAGTTTCATAGCCCATATATGAGGTTCCGCGTTACATACTTACG 1442
QY 517 GTAAATGGCCCGCTGGCTGACCGCCAAACGACCCCGCCCATTTGACGTCATATAATGACG 576
Db 1443 GTAAATGGCCCGCTGGCTGACCGCCAAACGACCCCGCCCATTTGACGTCATATAATGACG 1501
QY 577 TATGTTTCCCATAGTAAACGCAATAGGACTTTTCCATTGACGTCATATGGGTGGAGTATTTA 636
Db 1502 TATGTTTCCCATAGTAAACGCAATAGGACTTTTCCATTGACGTCATATGGGTGGAGTATTTA 1561
QY 637 CGGTAAACTGCCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTAT 695
Db 1562 CGGTAAACTGCCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTAT 1621
QY 696 TGAAGTCAATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTAGTACATGACCTTACGGGA 755
Db 1622 TGAAGTCAATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTAGTACATGACCTTACGGGA 1681
QY 756 CTTTCTCTACTCTGCGAGTACATCTAGTATTAGTTCATCGTATTACCATGCTGATCGGTT 815
Db 1682 CTTTCTCTACTCTGCGAGTACATCTAGTATTAGTTCATCGTATTACCATGCTGATCGGTT 1741
QY 816 TTGGCAGTACACCAATGGCGGTGGATAGCGGTTTGA CTCACGGGGATTTTCCAGTCTCCA 875
Db 1742 TTGGCAGTACACCAATGGCGGTGGATAGCGGTTTGA CTCACGGGGATTTTCCAGTCTCCA 1801

Db 3958 GCCTCTTTTCTATCTTCCAGGATATGAGGAAACAAATCATGCTTCAAAAACGTGGGC 4017
QY 3036 GGATCTCCCGTGTGTCTTGGCCAAAATTCGAGTCGCCAACCTCCCAATCACTCAC----- 3090
Db 4018 ACAGCTGATGAAAAGCTTCGAAAGAAATCATCATTTCTATCAATCATACCTCAGACGCACA 4077
QY 3091 CAACCTCTCTCTCCAAATTCCTGTTTCCTGTTATCGCTGGATGTTGCTGCGCGGTTTTATCA 3150
Db 4078 CAATCAATGGGAATACAACTGGACACAGAGATAATTTGTTATGTTTATGTTGCTGGGA 4137
QY 3151 TATTCCTCTTCACTCTGCTATGCTCATCTTCTTATTTGGTTCTTCGGATATCAAG 3210
Db 4138 AAGGAGCAGTGACAACCTTCACTTCGGTGATGACATGGATCCAGAGCTTCGTAGCCCTG 4197
QY 3211 GTATGTTGGCCGTTTGTCTCTAATTCAGGATCAACAACACAGTACGGGACCATGCA 3270
Db 4198 GCTCAGATCTTGATTCACAGAAAGTGAAGGAATCTCAACAGGAACTTATGAATTA 4257
QY 3271 AAACCTGACGACTCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGCTGTACAAAAC 3330
Db 4258 TAAGTACATAAATATATACTAATACTAATAAGTTAAGAAATACTAATCATTAGTTA 4317
QY 3331 CTACGATGGAATTCACCTGATTTCCATCCATCCATCGTCTGGGCTTTCGCAAAATACC 3390
Db 4318 ATAAGAATATAGATTTATTTGAATTAATCAATTAATAATTAAGTAAAGTTAACTAGTATT 4377
QY 3391 TATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTCACT 3450
Db 4378 AGTTAAGTTAGCTAATTTATATATGATTTGTCACAAATTAATGTAATCATTAAGCAAT 4437
QY 3451 GGTTCGTAGGGCTTTCCCACTGTTTGGCTTTTCACTATATGATGA-----TGTGTAAT 3507
Db 4438 CACTGCCATGTAATAACAGGGTATACGGGTGTTTTTTCATATGGGAAACAGGGTGGCTT 4497
QY 3508 GGGGCAAGTCTGTACATCGTCACTGCTTCTTGGCTTATACCGCTG----- 3552
Db 4498 AGGGCAGGTCACTTAAGTGACCTTTTGTATATATGATGATGATTTCAATTTGATC 4557
QY 3553 -----TACCAATTTTCTTGTCTCTGGGTAACATTTAAGAAATTCAGACTCGAGC 3603
Db 4558 GAATACTAATCTACTGCTCTCTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4617
QY 3604 AGTCTAGAA-----AGCGCGCAAGATATCAAGGATCCACTACGGTTAGAGC 3653
Db 4618 TCGTGCCGAATGGCGCGGATCTCGCAATCCCTAGAGGATTTAGGCAAGGGCTTTGAGC 4677
QY 3654 TCGC----- 3657
Db 4678 TCAGCTCTTGTGAGGACAGAAATACAAATCAGGGCAGTATATGAAATCTCATGAGAA 4737
QY 3658 -----TGATCAGCTCGACTGTGCTTCTAGTTGCGCAGCACTCTGTTGT 3701
Db 4738 AACCCAGATCTAGGTATGATCAGCTCGACTGTGCTTCTAGTTGCGCAGCACTCTGTTGT 4797
QY 3702 TTGCCCTCCCGTCTCTTGAACCTTGAAGGTGCCACTCCCACTGCTCTCTTCTCTA 3761
Db 4798 TTGCCCTCCCGTCTCTTGAACCTTGAAGGTGCCACTCCCACTGCTCTCTTCTCTA 4857
QY 3762 ATAAATGAGGAATTTGCATCGCATGCTGAGTAGGTGTCATTTCTTCTGGGGGTG 3821
Db 4858 ATAAATGAGGAATTTGCATCGCATGCTGAGTAGGTGTCATTTCTTCTGGGGGTG 4917
QY 3822 GTGGGGCAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGGATCTGTTGGGAGCT 3881
Db 4918 GGTGGGGCAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGGATCTGTTGGGATC 4977
QY 3882 CTT----- 3884
Db 4978 GGTGGGCTCTATGGCTTCTGAGCGGAAAGAACAGCTGGGGCTCGACAGCTCGACTCTA 5037
QY 3885 ---CCGCTTCTCGCTCACTGACTCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTAT 3941

Db 5038 GAATTCCTTCTCGCTCACTGACTCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTAT 5097
QY 3942 CAGCTCACTCAAAAGCGGTAATAACGTTTATCCAGAAATCAGGGGATAACGCAAGGAAGA 4001
Db 5098 CAGCTCACTCAAAAGCGGTAATAACGTTTATCCAGAAATCAGGGGATAACGCAAGGAAGA 5157
QY 4002 ACATGTGACAAAGGCGCAGCAAAAGGCGCAGGAAACCGTAAAAAGGCGGTGCTGCGCT 4061
Db 5158 ACATGTGACAAAGGCGCAGCAAAAGGCGCAGGAAACCGTAAAAAGGCGGTGCTGCGCT 5217
QY 4062 TTTTCCATAGGCTCGCGCCCTCGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGT 4121
Db 5218 TTTTCCATAGGCTCGCGCCCTCGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGT 5277
QY 4122 GCGCAAAACCGCAGGACTATAAAGATACAGGCGTTTCCCTCTGGAAGCTCCCTCTGTGC 4181
Db 5278 GCGCAAAACCGCAGGACTATAAAGATACAGGCGTTTCCCTCTGGAAGCTCCCTCTGTGC 5337
QY 4182 GCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGA 4241
Db 5338 GCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGA 5397
QY 4242 GGTGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGTCTGCTCGCT 4301
Db 5398 GGTGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGTCTGCTCGCT 5457
QY 4302 CCAAGCTGGCTGTGTGACGAAACCCCGTTCAGCCGACCGCTGCGCTTATTCGGTA 4361
Db 5458 CCAAGCTGGCTGTGTGACGAAACCCCGTTCAGCCGACCGCTGCGCTTATTCGGTA 5517
QY 4362 ACTATGCTTTCAGTCCAAACCGGTAAGACACGACTTATCGCACTGGGACGAGCCACTG 4421
Db 5518 ACTATGCTTTCAGTCCAAACCGGTAAGACACGACTTATCGCACTGGGACGAGCCACTG 5577
QY 4422 GTAAACAGGATTAGCAGAGGAGTATGTAGGCGGTGCTACAGAGTTCTTTGAAGTGTGGC 4481
Db 5578 GTAAACAGGATTAGCAGAGGAGTATGTAGGCGGTGCTACAGAGTTCTTTGAAGTGTGGC 5637
QY 4482 CTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 4541
Db 5638 CTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 5697
QY 4542 CCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCCGCTGGTAGCGGTG 4601
Db 5698 CCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCCGCTGGTAGCGGTG 5757
QY 4602 GTTTTTTTTGTTCGAAGCAGCAGATTACCGCGCAGAAAAAAGGATCTCAAGAGATCCTT 4661
Db 5758 GTTTTTTTTGTTCGAAGCAGCAGATTACCGCGCAGAAAAAAGGATCTCAAGAGATCCTT 5817
QY 4662 TGATCTTTTCTACGGGCTCTGACGCTCAGTGAAACGAAACCTCACTTAAAGGATTTGG 4721
Db 5818 TGATCTTTTCTACGGGCTCTGACGCTCAGTGAAACGAAACCTCACCTTAAAGGATTTGG 5877
QY 4722 TCATGAGATTATCAAAAGGATCTTCACCTAGTACCTTTTAAATTAATAATGAAGTTTA 4781
Db 5878 TCATGAGATTATCAAAAGGATCTTCACCTAGTACCTTTTAAATTAATAATGAAGTTTA 5937
QY 4782 AATCAATCTAAAGTATATATGATGATAAATTTGCTGACAGTTACCAATGCTTAATCAGTG 4841
Db 5938 AATCAATCTAAAGTATATATGATGATAAATTTGCTGACAGTTACCAATGCTTAATCAGTG 5997
QY 4842 AGGCACCTATCTCAGGATCTGCTATTTTCGTTTCATPCCATAGTTGCTGACTC 4894
Db 5998 AGGCACCTATCTCAGGATCTGCTATTTTCGTTTCATPCCATAGTTGCTGACTC 6050

RESULT 11
ACC71544
ID ACC71544 standard; DNA; 6148 BP.
XX
AC ACC71544;
XX

|||||
1277 ATACTCTGCTTTCAGAGACTGACACGGACTCTGTATTTTACAGGATGGGGTCCCATTT 1336
QY
1439 ATTATTTTACAAATTTACATATACAAACGCCGCTCCCGTCCCGCAGTGTATTTATTTAA 1498
Db
1337 ATTATTTACAAATTTACATATACAAACGCCGCTCCCGTCCCGCAGTGTATTTATTTAA 1396
QY
1499 CATAGCGTGGGATCTCC---GACATCTCGGGTACGTGTTCGGACATGGGCTTCTCCG 1555
Db
1397 CATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCGGACATGGGCTTCTCCG 1456
QY
1556 GTAGCGCGGAGCTCCACATCCGAGCCTGTGCTCCATCGCTCCAGCGCTCATGTGCG 1615
Db
1457 GTAGCGCGGAGCTCCACATCCGAGCCTGTGCTCCATCGCTCCAGCGCTCATGTGCG 1516
QY
1616 TCGCAGCTCTCTGCTCTAAACAGTGGAGCCAGACTTAAAGCACAGCAAAATGCCACCA 1675
Db
1517 TCGCAGCTCTCTGCTCTAAACAGTGGAGCCAGACTTAAAGCACAGCAAAATGCCACCA 1576
QY
1676 CCACAGTGTCCGCAACAGGCCGTGGCGGTAGGGTATGTGTCTGAAAATGAGCTCGGAG 1735
Db
1577 CCACAGTGTCCGCAACAGGCCGTGGCGGTAGGGTATGTGTCTGAAAATGAGCTCGGAG 1636
QY
1736 ATTGGGCTCGAC-CTGGAGCGAGATGGAAGACTTAAAGCAGCGGCAGAGAGATGCGAG 1794
Db
1637 ATTGGGCTCGACCGGCTGACGAGATGGAAGACTTAAAGCAGCGGCAGAGAGATGCGAG 1696
QY
1795 GCAGCTGAGTGTGTATTTCTGATAAGAGTCAAGAGTAACTCCCGTTGGCGTGTCTTAA 1854
Db
1697 GCAGCTGAGTGTGTATTTCTGATAGAGTCAAGAGTAACTCCCGTTGGCGTGTCTTAA 1756
QY
1855 CGGTGAGGCGAGTGTAGTCTGAGCAGTACTCGTTCTGCGCGCGGCCACACAGACATA 1914
Db
1757 CGGTGAGGCGAGTGTAGTCTGAGCAGTACTCGTTCTGCGCGCGGCCACACAGACATA 1816
QY
1915 ATAGCTGACAGACTACAGACTGTCTCTTCCATGGTCTTTTCTCGAGTCAACGTCGTC 1974
Db
1817 ATAGCTGACAGACTACAGACTGTCTCTTCCATGGGCTTTTCTCGAGTCAACGTCGAA 1876
QY
1975 GAC---GAATTCACAGCAATCATGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGTG 2030
Db
1877 TTCTCTAGCACTCGAAGCTTATGTCTTCAATGTAAGAAAGCTGGTCTAACAGATG 1936
QY
2031 CTGTGTGAGCAGTCTTCTGTTTCCCGCAGCGTAGCGAAACCAACGTC-ACCGGGGGAAG 2089
Db
1937 ACAACTAGAAACAAAGGCGAGGGGCCATCTGCGGCCACGACTCAAAACGACAGAATGCCA 1996
QY
2090 TCGCGGCCACACTGTGTCTGGATTGTGTAGCTCTCTCGCACAGGCGCCAAAGCAGAACGT 2149
Db
1997 GGCCTGTAGCTTTGGGCTGGATCTCTGAGCAGCTAATGACCGGAAGAAATTCCTGTAAAG 2056
QY
2150 CCAGCTGATCAACACCAACGGCAGTTGGCACTTCAATAGCAGCGCCCTGAACTGCAATGA 2209
Db
2057 GACATCTTCTGTATATTGAGAACAAATCCAGGATTAATGCTAGCACTCCCAAAATGCAACAA 2116
QY
2210 TAGCCTCAACACCGGCTGTGTGACGGGCTTTTCTATACCACAAGTTTCAATCTTTCAGG 2269
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2117 ACGAAGCCAAACCCGAAGACGCGCA---ACAGTCAAAACCCAAACGGACCCCAATTTGCAAT 2173
QY
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Db
2174 CATAGTTTGGAG----AGGTAGTACAACAATTTGGCTTCATTGGCTTCTGTTGTGCAAC 2228
QY
2330 TATCAGTTATGCCAAGCGAGCGCCCGACACAGCGCCCTACTGTGGCACTTACCCCCC 2389
Db
2229 AACAAACCATCGCATCAGAAATCATAGAACACGCAATTAAGAGTCTTGTGAATGGTCTAA 2288
QY
2390 AAAACCTTGGGTTATGTGCGCCGGAAGAGTGTGTGTGTCGGTATATTTGCTTCACTCC 2449
Db
2289 AGCCAGTTTATGATATGGCAAAACAAATCTCTCATTTGAACAGGGTTTGTGCTGAGATGG 2348
QY
2450 CAGCCCGTGTGTGGGAACGACAGGTCGGGCGCGCCACCTACAGCTGGGGTGA 2509
|||||

Db
2349 TTGCAAAATATGATCTTCTGGTGATGACAAACGGTCCGGCAACAGCAACCGCTGCGGCAA 2408
QY
2510 AAATGATACGAGCGTCTTCGTCTTTAAACAAATACCAAGGCACCGCTGGGCAAATTTGTTCCG 2569
Db
2409 CTGAGG-----CTTATTGGGCGGAACATGTGTCAACACCACTTGAGCAATCACTTTAT 2461
QY
2570 TTGTACTCTGGATGAATCAACTGGAATTCACAAAGTGTGGGAGCGCTCTTGTGTCTCAT 2629
Db
2462 GAAGAAGTGCATTTGGGGTAAGATTGAATCTAGAGATGAGACCGTCCC---TCAAAG 2517
QY
2630 CGAGGGGGCGGCAACACACCTGCATGCCCCACTGATTTGCTTCCGCAAGCATCCGGA 2689
Db
2518 TGTAGGAGGATTCACAAATCTAAACAGTACCACT----- 2554
QY
2690 CCGCACATATCTCTCGGTGGGCTCCCGTCCCTGGATTCACACCCAGGTGCTGTGTCGACTA 2749
Db
2555 --TCACTAATCAGGAAAAATTTTGGGAAACCTGCAATTTTCGGCAAGGATTTGAGAAACA 2612
QY
2750 CCGGTATAGGCTTTGGCATATCTCTGTATCATCACTACACTACACNATTTTAAATCAGGAT 2809
Db
2613 TTATGTATGATCACTTGCCTGTTTGGAACTGCTTTTCCACCAATTTAGTACAGTGAATTT 2872
QY
2810 GTACGTGGGAGGGTCAACACAGGCTGGAAGCTGCTTCAACTGACCGGGCGAAACG 2869
Db
2673 GTAAATTTGGGAAAAGATAGCAACTCATTTGGAATCATTTCTGATGAGTTCCAGGCCAGCC 2732
QY
2870 TTGCGATCTGGAAGATPAGGACAGGTCGAGATCGATATGGAACATCACATCAGGATTT 2929
Db
2733 TGGCTGAAGGAGACTCTCTCAATGTGCCCTAATTCNAATTAACAAAAGATTTCCAATCT 2792
QY
2930 CCTAGACCCCTGCTGCTGTGTACAGCGGGGTTTCTTGTGTGACAGAAATCCTCACAAT 2989
Db
2793 TCCAAGATCTGCTCATCTGTCCACATCCGCTTTTCAGGTGACATTTCCCGAGCTT 2852
QY
2990 ACGCAGAGCTTAGACTCGTGGTGA-CTTCTCTCAATTTTCTAGGGGATCTCCCGTGT 3048
Db
2853 GCAGAAAAGCTTGGCTCAGTCCCAACCATCGCCCAAGATTTGATCAGGTTGGGATGTGT 2912
QY
3049 GTCTTGGCCAAATTTGG---CAGTCCCCAACCTTCAATCACTACCAACCTCTCTGTCTC 3105
Db
2913 TTTTCAGCTTCAAGATGGTAAACACTTGGACTCAAAATTTGAGCCCAATCTCCCTTCCCT 2972
QY
3106 CAATTTGCTCTGTTATCGCTGATGTGTCGGGGTTTTATCATATTTCTCTTCTTCACTCC 3165
Db
2973 CCGAAAGGCGGAATAATAGCAGAGCTTCAACTGCTGAACTATAGGGTACGTTACAT-- 3030
QY
3166 TGCTGTATGCTCATCTTCTTATTTGTTTCTTCTGATTTATCAAGTATTTGTGCGCGCTTT 3225
Db
3031 -----TAAATGATACACTTGTGATATCAGCCCTGGATAATATAAGTCAATTAACGACC 3084
QY
3226 GTCTCTAATTTCCAGGATCAACAAACAGTACGGGACATGCAAAAACCTGACCACTC 3285
Db
3085 AAGATAAAATTTGTTTCATATCTCGTAGCAGCTTAAATAATAAATGTAATAGGAGCTATAT 3144
QY
3286 CTGCTCAAGCAACTCATATGTTTCCCTCATGTTGTGTGTAACAAAACCTACGGATGGAATTT 3345
Db
3145 CTCTGACAGGGGATCCAGATCTGCTGTGCTCTTCTAGTTGCCAGC----- 3189
QY
3346 GCACCTGTATTTCCCATCCCATGCTCTGGGCTTTTCGCAAAAATACCTATGAGGAGTGGGCT 3405
Db
3190 ---CATCTGTTTGGCCCTCCCGTGCCTTCTTTCAGCCCTGGAAAGGTGCCACTCCCA 3246
QY
3406 CAGTCTGTTTCT-CTTGGCTCAGTTTATAGTGGCCATTTGTTTTCAGTGGTTCGTAGGGCTT 3464
Db
3247 CTGTCTTTCTTAATAAATGAGAAATTTGCATCGAATTTGTCTGAGTAGGTGTCTTCTA 3306
QY
3465 TCCCCCCTGTTTGGCTTTTTCAGCTATGATGATGTGTATTTGGGGCCCAAGTCTGTAC 3524
Db
3307 TTTCTGGGGGGTGGGGTGGGGGACAGACAGAGGGGGAGGATTTGGGAAGACAATAGCAGGC 3366
QY
3525 AGCATCGTGAAGTCCCTTTTATACCGCTGTTTACCAATTTTCTTTTGTCTCTGGGTATACAT 3584
Db
3367 ATGCTGGGATGCGGTGGGCTCTATGGGTACCCAGGTGCT-----GAAGAATTG 3415

QY 3585 TAAGAAATTCAGACTCGAGCAAGTCTAGAAAGCGCGCAAGATATCAAGGATCCACTACG 3644
DB |||||
3616 ACCCGGTTCTCTCGCGCGCAAGAGAGCAGCACATCCCTCTCTGTGACACACCGCTG 3475
QY 3645 CGTTAGAGCTCGCTGATCAGCCTCGATGTGCGCTTCTAGTTGCGACGCATCTGTGTTTG 3704
DB |||||
3676 TCCAGCGCCCTGTTCTTAGTTCCAGCCCACTCATAGGACACTCATAGCTCAGGAGGCG 3535
QY 3705 CCCCTCCCGCTGCTTCTGACCCCTGGAAGTGCCACTCCCACTGCTCTCTTCTTAATA 3764
DB |||||
3536 TCCGCTTCAATCCCAACCCGCTAAGTACTTGGAGCGGCTCTCTCCCTCATCAGCCC 3595
QY 3765 AAATGAGGAAATGCATCGCATGTTCTGAGTAGTGTCATTCTATTTCTGGGGGGTGGGGT 3824
DB |||||
3596 ACCAAACCAACCTAGCTCCAGAGTGGGAGAAATTAAGCAAGATAGGCTATTAAGT 3655
QY 3825 GGGCAGGACAGCAAGGGG---GAGGATTTGGGAAGACAATAGCAGGCAATGCTGGGGAGCT 3881
DB |||||
3656 GCAGAGGAGAGAGAAATGCTCCCAACATGTGAGGAAGTAATGAGAGAAATCATAGAAATTT 3715
QY 3882 CTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3941
DB |||||
3716 CTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3775
QY 3942 CAGCTCACTCAAAGCGGTAATACGTTATCCAGAAATCAGGGGATAAGCGAGGAAGA 4001
DB |||||
3776 CAGCTCACTCAAAGCGGTAATACGTTATCCAGAAATCAGGGGATAAGCGAGGAAGA 3835
QY 4002 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCCGCTGCTGCGCT 4061
DB |||||
3836 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCCGCTGCTGCGCT 3895
QY 4062 TTTTCCATAGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGT 4121
DB |||||
3896 TTTTCCATAGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGT 3955
QY 4122 GGGCAAAACCGCAGGACTATAAGATACAGGGGTTTCCCTCGAAGCTCCCTCGTGC 4181
DB |||||
3956 GGGCAAAACCGCAGGACTATAAGATACAGGGGTTTCCCTCGAAGCTCCCTCGTGC 4015
QY 4182 GCTCTCTGTTCGACCCCTGCGCTTACCGGATACCTGTCGCTTTCTCCCTCGGGAA 4241
DB |||||
4016 GCTCTCTGTTCGACCCCTGCGCTTACCGGATACCTGTCGCTTTCTCCCTCGGGAA 4075
QY 4242 GCGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTCGCT 4301
DB |||||
4076 GCGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTCGCT 4135
QY 4302 CCAAGCTGGGCTGTGTCAGCAACCCCGTTACGCGCCGACCGCTGCGCTTATCCGGTA 4361
DB |||||
4136 CCAAGCTGGGCTGTGTCAGCAACCCCGTTACGCGCCGACCGCTGCGCTTATCCGGTA 4195
QY 4362 ACTATCGTCTGTAGTCAACCCCGTAAAGACAGCACTTATCCCACTGGCAGGACCACTG 4421
DB |||||
4196 ACTATCGTCTGTAGTCAACCCCGTAAAGACAGCACTTATCCCACTGGCAGGACCACTG 4255
QY 4422 GTAACAGATATGACAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTCAAGTGTGGC 4481
DB |||||
4256 GTAACAGATATGACAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTCAAGTGTGGC 4315
QY 4482 CTAAGCTGGCTCACTAGAGGACAGTATTGTTGATCTGCGCTCTGCTCAAGCCAGTTA 4541
DB |||||
4316 CTAAGCTGGCTCACTAGAGGACAGTATTGTTGATCTGCGCTCTGCTCAAGCCAGTTA 4375
QY 4542 CTTTCGAAAAAGAGTTGGTAGCTTTGATCCGCAAAACCAACCGCTGGTAGCGGTG 4601
DB |||||
4376 CTTTCGAAAAAGAGTTGGTAGCTTTGATCCGCAAAACCAACCGCTGGTAGCGGTG 4435
QY 4602 GTTTTTTTTGTGAACGACAGAGTTACGGCGAGAAAAAAGGATCTCAGAGAGATCCTT 4661
DB |||||
4436 GTTTTTTTTGTGAACGACAGAGTTACGGCGAGAAAAAAGGATCTCAGAGAGATCCTT 4495

QY 4662 TGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTGG 4721
DB |||||
4496 TGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTGG 4555
QY 4722 TCATGAGATTATCAAAAGGATCTTACCTAGATCTTTTAAATTAATAATGAAGTTTAA 4781
DB |||||
4556 TCATGAGATTATCAAAAGGATCTTACCTAGATCTTTCCTTTTAAATTAATAATGAAGTTTAA 4615
QY 4782 AATCAATTAAGTATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTG 4841
DB |||||
4616 AATCAATTAAGTATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTG 4675
QY 4842 AGGCACCTATCTCAGCGATCTGTATTTCGTTTCATCCATAGTTGCTGACTCC 4895
DB |||||
4676 AGGCACCTATCTCAGCGATCTGTATTTCGTTTCATCCATAGTTGCTGACTCC 4729

RESULT 12
ACC71554
ID ACC71554 standard; DNA; 6258 BP.
XX
AC ACC71554;
XX
DT 10-JUL-2003 (first entry)
XX
VRC6801 (pVR1012x/s Lassa GP (dtm) plasmid.
XX
Virucide; vaccine; immune response; Ebola virus; Marburg virus;
XX Lassa virus; retrovirus; paramyxovirus; influenza virus; adenovirus;
XX viral infection; filovirus; circular; cyclic; ds.
XX Synthetic.
XX
XX WO2003028632-A2..
XX
XX 10-APR-2003.
XX
XX 24-SEP-2002; 2002WO-US030251.
XX
XX 01-OCT-2001; 2001US-0326476P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Nabel GJ, Yang Z, Sullivan N, Sanchez A;
XX
XX WPI; 2003-371961/35.
XX
XX New bimodal priming and boosting compositions, useful as viral vaccines,
XX PT specifically for eliciting an immune response against a filovirus or a
XX disease caused by infection with filovirus.
XX
XX Claim 1; Page 195-197; 219pp; English.
XX
XX The present invention relates to a bimodal priming composition and
XX CC boosting composition for priming and boosting an immune response to an
XX CC antigen in an individual. The compositions comprise (a) a priming
XX CC composition comprised of a DNA plasmid comprising a nucleic acid molecule
XX CC encoding Ebola, Marburg, Lassa, retrovirus, paramyxovirus or influenza
XX CC virus glycoprotein or nucleoprotein or their epitope-bearing domain, or a
XX CC DNA plasmid selected from ACC71521-ACC71563 and (b) a boosting
XX CC composition comprised of a replication-deficient adenovirus, comprising a
XX CC nucleic acid molecule encoding Ebola, Marburg, Lassa, retrovirus,
XX CC paramyxovirus, or influenza virus glycoprotein or nucleoprotein or
XX CC epitope-bearing domain, or a replication deficient adenovirus selected
XX CC from constructs ACC71521-ACC71563. The compositions are useful as viral
XX CC vaccines, specifically for eliciting an immune response against a
XX CC filovirus or a disease caused by infection with filovirus e.g. Ebola
XX CC virus infection
XX
SQ Sequence 6258 BP; 1674 A; 1494 C; 1476 G; 1614 T; 0 U; 0 Other;
Query Match 40.2%; Score 2363; DB 10; Length 6258;
Best Local Similarity 70.6%; Pred. No. 1.4e-244;

Matches 3498; Conservative 0; Mismatches 1280; Indels 177; Gaps 19;

QY	1	TCGCGCGTTTCGGTGATGACGGTGAAACCTCTGACACATGCAAGCTCCCGGAGACGGTCA	60
Db	1	TCGCGCGTTTCGGTGATGACGGTGAAACCTCTGACACATGCAAGCTCCCGGAGACGGTCA	60
QY	61	CAGCTTGTCTGTAAGCGGATGCGGAGCAGACAAAGCCGTCAGGCGGCTCAGCGGCTG	120
Db	61	CAGCTTGTCTGTAAGCGGATGCGGAGCAGACAAAGCCGTCAGGCGGCTCAGCGGCTG	120
QY	121	TTGGCGGGTGTCCGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGACTCAGAGTGC	180
Db	121	TTGGCGGGTGTCCGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGACTCAGAGTGC	180
QY	181	ACCATATGAAGCTTTTGGAAAAGCCTAGGCTCCAAAAAGCCCTCCTCACTACTTCTGG	240
Db	181	ACCATATGGG-----TGTGAAATACCGCAC	207
QY	241	AATAGCTCAGAGCCGAGGCGGCTCGGCTCTGCTATATAAATAAAAAAATTAGTCAGCCA	300
Db	208	GATGCGTAAGGAGAAATACCGCATCAG-----	235
QY	301	TGGGCGGAGAAATGGGCGGAACTGGGCGGAGGGAATTATTGGCTATTGGCCATTGCAAT	360
Db	236	-----ATTGGCTATTGGCCATTGCAAT	256
QY	361	ACGTTGTATCTATCATATAATATGTAATTTATATTGGCTCATGTCCAATATGACCGCCA	420
Db	257	ACGTTGTATCCATATCATATAATATGTAATTTATATTGGCTCATGTCCAATATGACCGCCA	316
QY	421	TGTTGACATTGATTATTGACTAGTATTAACTAGTAATCAATTACGGGTCATTAGTTTCAT	480
Db	317	TGTTGACATTGATTATTGACTAGTATTAACTAGTAATCAATTACGGGTCATTAGTTTCAT	376
QY	481	AGCCCATATATGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCTGCTGACCG	540
Db	377	AGCCCATATATGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCTGCTGACCG	436
QY	541	CCCAACGACCCCGCCCATATGACGTCATTAATGACGTTATGTTCCCATAGTAAGCCCAATA	600
Db	437	CCCAACGACCCCGCCCATATGACGTCATTAATGACGTTATGTTCCCATAGTAAGCCCAATA	496
QY	601	GGGACTTTCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACATTTGGCAGTA	660
Db	497	GGGACTTTCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACATTTGGCAGTA	556
QY	661	CATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCATTAAGCAGGTAAATGGCCC	720
Db	557	CATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCATTAAGCAGGTAAATGGCCC	616
QY	721	GCCTGGCAATTATGCCAGTACATGACCTTACGGGACTTTTCCTACTTTGGCAGTACATCTAC	780
Db	617	GCCTGGCAATTATGCCAGTACATGACCTTATGGGACTTTTCCTACTTTGGCAGTACATCTAC	676
QY	781	GTATTAGTCAATCCGCTATTACATGGGTGATCGCGTTTGGCAGTACACCAATGGCGTGA	840
Db	677	GTATTAGTCAATCCGCTATTACATGGGTGATCGCGTTTGGCAGTACACCAATGGCGTGA	736
QY	841	TAGCGGTTTGACTCAGCGGGAATTTCCAAGTCTCCACCCATTTGACCTCAATGGGAGTTTG	900
Db	737	TAGCGGTTTGACTCAGCGGGAATTTCCAAGTCTCCACCCATTTGACCTCAATGGGAGTTTG	796
QY	901	TTTTGGGACCAAAATCAACCGGACTTTCCAAAATGTCGTAATAAACCCCGCCCGTTGACG	960
Db	797	TTTTGGGACCAAAATCAACCGGACTTTCCAAAATGTCGTAATAAACCCCGCCCGTTGACG	856
QY	961	CAATGGGCGGTAGGCGTGTACCGTGGAGTCTATATAGCAGAGCTCGTTTAGTGAAC	1020
Db	857	CAATGGGCGGTAGGCGTGTACCGTGGAGTCTATATAGCAGAGCTCGTTTAGTGAAC	916
QY	1021	CGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGAC	1080
Db	917	CGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGAC	976

QY	1081	CGATCCAGCCTCCGCGGCCGGAAACGGTGCATTGGAAACGGGATTCCTCCGTCGCAGAGT	1140
Db	977	CGATCCAGCCTCCGCGGCCGGAAACGGTGCATTGGAAACGGGATTCCTCCGTCGCAGAGT	1036
QY	1141	GACGTAAGTACCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGATGCTATA	1200
Db	1037	GACGTAAGTACCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGATGCTATA	1096
QY	1201	CTGTTTTTGGCTTGGGGCCTATACACCCCGCG-TCCTTATGCTATATAGGTGATGTTATAG	1259
Db	1097	CTGTTTTTGGCTTGGGGCCTATACACCCCGCTATGCTATGCTATATAGGTGATGTTATAG	1156
QY	1260	TTAGCCTATAGGTGCGGTTATTGACCATATTAGCCACTCCCTTATTTGGTGAAGTACT	1319
Db	1157	TTAGCCTATAGGTGCGGTTATTGACCATATTAGCCACTCCCTTATTTGGTGAAGTACT	1216
QY	1320	TTCCATTACTAATCCATAACATGGCTTTGGCCACAACCTATCTTATTTGGCTATATGCCA	1379
Db	1217	TTCCATTACTAATCCATAACATGGCTTTGGCCACAACCTATCTTATTTGGCTATATGCCA	1276
QY	1380	ATACTCTGCTTCAGAGACTGACACGGACTCTGTAATTTTTACAGGATGGGT-CCATTT	1438
Db	1277	ATACTCTGCTTCAGAGACTGACACGGACTCTGTAATTTTTACAGGATGGGTCCCATTT	1336
QY	1439	ATTATTTACAAATTCACATATACACACCGCGTCCCGCTGCCCGCAGTTTTTATAA	1498
Db	1337	ATTATTTACAAATTCACATATACACACCGCGTCCCGCTGCCCGCAGTTTTTATAA	1396
QY	1499	CATAGCTGGGATCTCC--GACATCTCGGGTACGTTTCCGGACATGGGCTCTTCTCG	1555
Db	1397	CATAGCTGGGATCTCCAGCGGAATCTCGGTAAGTGTTCGGACATGGGCTCTTCTCG	1456
QY	1556	GTAGCGCGGAGCTTCCACATCCGAGCCCTGTCCTCATCCGTCAGCGCTCATGTGCG	1615
Db	1457	GTAGCGCGGAGCTTCCACATCCGAGCCCTGTCCTCATCCGTCAGCGCTCATGTGCG	1516
QY	1616	TGGGAGCTCTTCTCTTAAAGTGGAGCCAGACTTGGGACACAGCAATGCCACCA	1675
Db	1517	TGGGAGCTCTTCTCTTAAAGTGGAGCCAGACTTGGGACACAGCAATGCCACCA	1576
QY	1676	CCACAGTGTGCGCACAAAGCGCGTGGCGGTAGGGTATGTCTGAAAAATGAGCTCGGAG	1735
Db	1577	CCACAGTGTGCGCACAAAGCGCGTGGCGGTAGGGTATGTCTGAAAAATGAGCTCGGAG	1636
QY	1736	ATTGGGCTCGCAC-CTGGACCGCAGATGGAAGACTTAAAGCAGCGGCGAGAAAGATGCAG	1794
Db	1637	ATTGGGCTCGCACCGCTGACGAGATGGAAGACTTAAAGCAGCGGCGAGAAAGATGCAG	1696
QY	1795	GCAGCTGAGTTCTGTTATTTCTGATAGAGTCAAGGTAACTCCGTTGCGGTCTCTTAA	1854
Db	1697	GCAGCTGAGTTCTGTTATTTCTGATAGAGTCAAGGTAACTCCGTTGCGGTCTCTTAA	1756
QY	1855	CGGTGAGGCGAGTGTAGTCTGACAGTACTCGTTGCTCGCGCGCGCCACACAGACATA	1914
Db	1757	CGGTGAGGCGAGTGTAGTCTGACGAGTACTCGTTGCTCGCGCGCGCCACACAGACATA	1816
QY	1915	ATAGCTGACAGACTAACAGACTGTTCTTTTCAATGGGTCTTTTCTGCACTACCGTCGTC	1974
Db	1817	ATAGCTGACAGACTAACAGACTGTTCTTTTCAATGGGTCTTTTCTGCACTACCGTCGTC	1876
QY	1975	GAGGAATTCAGCAATCATGGATGCG---AATGAGAGAGGGCTCTGCTGTGCTGCTG	2030
Db	1877	GACAGTGTGATCAGATATCGCGGCGCTCTAGAAATTTAGGATTTGGCTTTAGAGATTC	1936
QY	2031	CTGTGTGGAGCAGTCTTCTGTTTCCGCGCAGCGCTAGCGAAACCCACGCTACCGGGGAAGT	2090
Db	1937	ACTACTAGTTAGGAATTCCTAAATCATGGGCGAGATTAATACATTTCTTTCAAGAGTGC	1996
QY	2091	GCGGCGCACATGTGTCTGGATTGTTAGC-CTCTCTGCGACGAGGCGCCACAGAACGTT	2149
Db	1997	ACATGTAATAGGGAAGTCAAGCAATTTGTCTAATTTGGCTTTCTCTATTATGGCAATCTT	2056

Qy	2150	CCAGCTGATCAACACCAACGGCAGTTGGACACCTCAATAGCAGCGCCCTGAACATGC	2209
Db	2057	GAAGGGCTTGTAATCAACATCGCTACATGTGGGAATTAITGGATGTGGTTCCTTTTATTC	2116
Qy	2210	TAGCCTCAACACACGGCTGGTTGGCAGGCGTTTCTATACACACAAGTTCAACTCTTCAGG	2269
Db	2117	GTGTGGCAAGTCTTGTTCCCTTAACCCCTTAAGGGGGATATGAGCTGCAACCTTAGA	2176
Qy	2270	CTGTCTAGAGAGCTAGCCAGCTGCGACCCCTTACCGATTTTGAACAGGGCTGGGGCCC	2329
Db	2177	AAATATGGAGAGCCCTAAACATGACCATGCCCCTTATCATGCACCAAGAAACGACGATCATCA	2236
Qy	2330	T---ATCAGTTATGCCAACGGAAGCGGCCGCCAGCAGGC---CCCTACTGCTGGCACTA	2383
Db	2237	TTACATAAGAGTGGGCAATGAGACTGGAATTAGAATTGACTTTAACTAAACACCAAGCATTAT	2296
Qy	2384	CCCCCAAAACCTTGGCGGTATTTGGCCGGAGAGAGTGTGTGGTCCGGTATATTGCTT	2443
Db	2297	AAATCACAAAATTTTGCAACTTATCCGATGCTCAAAAAAGAACTTTTATGATCATGCTCT	2356
Qy	2444	CACCTCCAGCCCGTGGTGGTGGGAACGACCGACAGGTGGGGCGGCCCACTACAGCTG	2503
Db	2357	CATGAGCATCATCTCAACATTTCCATCTATCCATTTCCAAACTTCAATCAGTATGAGCCAT	2416
Qy	2504	GGGTGAAAATGATACGAGAGTCTTGTGCTTTAACAATACAGGCGACCGCTGGGCAATTG	2563
Db	2417	GAGTTGTGATTTCAATGGAGGGAATAACAGTGTGCTCAATAACCTCTCTCATTTCTTATGC	2476
Qy	2564	GTTCCGGTTGTACCTGGATGAACCAACTGGATTTCAACAAAGTGTGGGAGGGCCTCCTTG	2623
Db	2477	TGGGGAATGGGCGCAACACTGTGGGAAGTTGCCAACGGAGTGTGCAAAACATTTATGAG	2536
Qy	2624	TGTCATCCGAGGGCGGGCAACCAACCTGCACTGCCCACTGATTTGCTTCGCGCAAGCA	2683
Db	2537	AATGGCTCGGGTGGAGATACATTTGCAATTAGACTCAGGAAGAGGAACTGGGACTGTAT	2596
Qy	2684	TCCGGACGCCACATCTCTCGTGGCGGCTCGGTCCCTGGATCACACCCAGGTGCTCTGGT	2743
Db	2597	AATGACCAGCTACCCAGTACCTGATTAATCAAAATACAACTGGGAGGACCACTGCCAA	2656
Qy	2744	CGACTACCCGTATAGGCTTTGG--CATTATCCTGTGTACCATCAACTACACCATATTTAA	2801
Db	2657	CTCAAGACCGTCTCCTATCGGGTACCTTGGCCTTTGTCAAAAGGCAAGAGATATATA	2716
Qy	2802	ATCAGGATGTACGTGGGAGGGTCCGAACACAGGCTGGAAGCTGCTCGCAACTCGACGCGG	2861
Db	2717	TATTAAGTAGAGGCTCTTGGGACCTTCAC-----CTGGACATTTGTAGATTCTG	2766
Qy	2862	GGCGAAGTTGCCATCTGGAAGATAGGGAAGGTCGAGATCGATATGGAGAACATCACA	2921
Db	2767	AGGCAATGAACACACAGGTGGTTATTGTTTAACACAGGTGGATGCTAAATGAAGCAGA	2826
Qy	2922	TCAGGATTCCTAGGACCCCTGCTCGTGTATACGGCGGGTTTTTCTGTGTGACAGAATC	2981
Db	2827	TCAAGTGTTTGGGAATACAGCTGTGCAAAATGCAATGAGAAGCATGATGAGGAGTTTT	2886
Qy	2982	CTCAACAATACGCGAGTCTAGACTCGTGTGTGACTTCTCTCAATTTTCTAGGGGATCT	3041
Db	2887	GTGACATCTGAGATTGTTGATTTTCAACAGCAAGCAATCCGTAGGTTGAGGCTGAGG	2946
Qy	3042	CCCGTGTGCTTGGCCAAAATTCGAGTCCCCCACTCCAAATCACTACCAACCTCCTGT	3101
Db	2947	CCCAGATGAGTATTCAATTAATAAATAAGCCGTGAATGCTTAAATCAATGATCAATTA	3006
Qy	3102	CCTCCA-----ATTGTCTCTGGTTATCGCTGATGTGTCGGGGTTTTAT	3148
Db	3007	TCATGAAGAACCAATTTAAGAGACATCATGGGCATTCCTCTACTCCAAATACAGCAAGTAT	3066
Qy	3149	CATATTCCTCTTCATCTCGTGTATGCCCTCATCTCTTATTTGTTCTCTCTGATTATCA	3208
Db	3067	GGTACCTTAATCATCTAGTAGCGGGAACAATCACTAACAAAGTGTGGCTTATATCCA	3126
Qy	3209	AGGTATGTTGCCGCTTTGTCTCTTAATTCAGGATCAACAAACCAACGATACGGGACCATG	3268

Db 6025 ||||| AGTCTGTCCTCAAGCTGGCTGTGTGCAGAACCCCGCTTCAGCCGACCGTGGC 6084
Qy 4350 CTTTATCCGCTAACTATCGTCTTGAGTCCAAACCGGTAAGACACGACTTATCCGCACTGG 4409
Db 6085 CTTTATCCGCTAACTATCGTCTTGAGTCCAAACCGGTAAGACACGACTTATCCGCACTGG 6144
Qy 4410 CAGCAGCACTGGTAAACAGAGTATAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCT 4469
Db 6145 CAGCAGCACTGGTAAACAGAGTATAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCT 6204
Qy 4470 TGAAGTGGTGGCTTAACCTACGCTACACTAGAGGACAGATTTGGTATCTCGGCTCTGC 4529
Db 6205 TGAAGTGGTGGCTTAACCTACGCTACACTAGAGGACAGATTTGGTATCTCGGCTCTGC 6264
Qy 4530 TGAAGCAGTACTCTCGGAAAAGAGTTGCTAGCTCTTCATCCGGCAAAACCAACCCG 4589
Db 6265 TGAAGCAGTACTCTCGGAAAAGAGTTGCTAGCTCTTCATCCGGCAAAACCAACCCG 6324
Qy 4590 CTGGTACGGTGGTTTTTTTGTGCAAGCAGCAGATTAACGCGCAGAAAAAAGGATCTC 4649
Db 6325 CTGGTACGGTGGTTTTTTTGTGCAAGCAGCAGATTAACGCGCAGAAAAAAGGATCTC 6384
Qy 4650 AAGAAGATCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGACGAAAACTCAGTT 4709
Db 6385 AAGAAGATCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGACGAAAACTCAGTT 6444
Qy 4710 AAGGATTTTGGTCATCAGATTAACAAAAAGGATCTTCACCTAGATCTTTTAAATTA 4769
Db 6445 AAGGATTTTGGTCATCAGATTAACAAAAAGGATCTTCACCTAGATCTTTTAAATTA 6504
Qy 4770 AATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAAT 4829
Db 6505 AATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAAT 6564
Qy 4830 GCTTAATCAGTGAGGCACTATCTCAGCGATCTGTCTATTTCGTTTCAATCATAGTTGCCT 4889
Db 6565 GCTTAATCAGTGAGGCACTATCTCAGCGATCTGTCTATTTCGTTTCAATCATAGTTGCCT 6624
Qy 4890 GACTCCCGTCGTGTAGATAACTACGATACGGAGGGCTTACCATCTGGCCCGAGTGGTG 4949
Db 6625 GACTCCCGTCGTGTAGATAACTACGATACGGAGGGCTTACCATCTGGCCCGAGTGGTG 6684
Qy 4950 CAATGATACCGCAGAGACCCAGCTCACCGCTCCAGATTTATCAGCAATAAACCCAGCCAG 5009
Db 6685 CAATGATACCGCAGAGACCCAGCTCACCGCTCCAGATTTATCAGCAATAAACCCAGCCAG 6744
Qy 5010 CCGGAAGGCGCAGCGCAGAGTGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTA 5069
Db 6745 CCGGAAGGCGCAGCGCAGAGTGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTA 6804
Qy 5070 ATTGTTGCCGGAAGCTAGAGTAGTTTCGCCAGTTAATAGTTTGGCAACGTTGTTG 5129
Db 6805 ATTGTTGCCGGAAGCTAGAGTAGTTTCGCCAGTTAATAGTTTGGCAACGTTGTTG 6864
Qy 5130 CCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGTATGGCTTCATTTCAGTCCG 5189
Db 6865 CCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGTATGGCTTCATTTCAGTCCG 6924
Qy 5190 GTTCCCAACGATCAAGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCT 5249
Db 6925 GTTCCCAACGATCAAGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCT 6984
Qy 5250 CTTCCGCTCTCCGATCGTTGTAGAGTAAGTTGGCCGAGTTATCATCTCATGTTA 5309
Db 6985 CTTCCGCTCTCCGATCGTTGTAGAGTAAGTTGGCCGAGTTATCATCTCATGTTA 7044
Qy 5310 TGGCAGCACTGCATAATCTCTTACTGTCAATCCGTAAGATGCTTTCTGTGACTG 5369
Db 7045 TGGCAGCACTGCATAATCTCTTACTGTCAATCCGTAAGATGCTTTCTGTGACTG 7104
Qy 5370 GTGAGTACTCAACCAAGTCAATCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGGC 5429
|||||

Db 7105 GTGAGTACTCAACCAAGTCAATCTGAGAAATAGTGTATGCGGCGACCGAGTTGCTCTTGCC 7164
Qy 5430 CGCGCTCAATACAGGGATAATACCGGCCACATAGCAGAACTTTAAAGTGTCTCATATTG 5489
Db 7165 CGCGCTCAACAGGGATAATACCGGCCACATAGCAGAACTTTAAAGTGTCTCATATTG 7224
Qy 5490 GAAAAAGTCTTCTCGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTGCA 5549
Db 7225 GAAAAAGTCTTCTCGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTGCA 7284
Qy 5550 TGTAAACCACTCGTGACCACTGATCTTCAAGCATCTTTTACTTTTCAACAGGTTTCTG 5609
Db 7285 TGTAAACCACTCGTGACCACTGATCTTCAAGCATCTTTTACTTTTCAACAGGTTTCTG 7344
Qy 5610 GGTGACAAAAACAGGAAGCAAAATGCCGCAAAAAAGGAATAAGGGCGACACGGAAT 5669
Db 7345 GGTGACAAAAACAGGAAGCAAAATGCCGCAAAAAAGGAATAAGGGCGACACGGAAT 7404
Qy 5670 GTTGAATACATACATCTTCTCTTTTCAATATTTTGAAGCATTTTATCAGGGTTATTGTC 5729
Db 7405 GTTGAATACATACATCTTCTCTTTTCAATATTTTGAAGCATTTTATCAGGGTTATTGTC 7464
Qy 5730 TCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGTTCCGCGCA 5789
Db 7465 TCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGTTCCGCGCA 7524
Qy 5790 CATTTCCCGAAAAAGTGCCACCTGACGCTCTAAGAAACCATTTATTCATGACATTAACCT 5849
Db 7525 CATTTCCCGAAAAAGTGCCACCTGACGCTCTAAGAAACCATTTATTCATGACATTAACCT 5884
Qy 5850 ATAAAAATAGGCGTATCACGAGGCCCTTTCGTC 5982
Db 7585 ATAAAAATAGGCGTATCACGAGGCCCTTTCGTC 7617
RESULT 15
ABK91498
ID ABK91498 standard; DNA; 6577 BP.
XX
AC ABK91498;
XX
XX
DT 14-AUG-2002 (first entry)
XX
DE Modified HIV protein-encoding plasmid DNA #50.
XX
KW HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV;
KW Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS;
KW acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
XX
OS Synthetic.
XX
PN WO200232943-A2.
XX
PD 25-APR-2002.
XX
PF 14-AUG-2001; 2001WO-US025721.
XX
PR 14-AUG-2000; 2000US-0225097P.
PR 14-NOV-2000; 2000US-0252115P.
PR 28-MAR-2001; 2001US-0279257P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
XX
XX Nabel GJ, Huang Y;
PI
XX
XX WPI; 2002-454594/48.
XX
XX New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and
PT its encoded protein, useful as vaccines for genetic or protein
PT immunization for acquired immunodeficiency syndrome or human
PT immunodeficiency virus infection.
XX

Db 1757 CGGTGAGGCGAGTGTAGTCTGAGCAGTACTCGTGTGCTCGCGCGCGCCACAGACATA 1816
Qy 1915 ATAGCTGACAGACTAAACAGACTGTCTCTTTCCATGGGTCTTTTCTGCACTCAGTCACGTCGTC 1974
Db 1817 ATAGCTGACAGACTAAACAGACTGTCTCTTTCCATGGGTCTTTTCTGCACTCAGTCACGTCGTC 1876
Qy 1975 GACGAATTTCAAGCA---ATCATGATGCAATGAAGAGAGGGCTCTGCTGTGCTGCTGTC 2031
Db 1877 GACACGTGTGATCAGATATCGCGCGCTCTAGACACCATGCTGCGTGAAGGAGAAATACC 1936
Qy 2032 TGTGTGGAGCAGTCTTCTGTTTCCGCCAGCGCTAGCGNAACCCACGTCACCGGGGAGTG 2091
Db 1937 AGCACCTGTGGCGTGGCGTGGCGTGGCGCCACATGCTGTGGGATGCTGATGATCT 1996
Qy 2092 CCGGCCACACTGTGTCTGATTTTGTAGCTCTCTCGCACCGAGCGCGCCCAAGCAGAACTGCC 2151
Db 1997 GCAGCGCCACGAGC-----TAGCAGCTTGAAGTGCACCGGACCTGGAAGACGACA 2047
Qy 2152 AGCTGATCAACACAAACGCGAGTTGGCACTCAATAGCACGCGCCCTGAACTGCAATGATA 2211
Db 2048 CCAACACCAACAGCAGCGCGCGCATGATCATGGAGAGGGCGAGATCAAGAACTGCA 2107
Qy 2212 GCCTCAACACCGGCTGTTGGAGGGCTTTTCTATCACCAAGTTCAACTCTTCAGGCT 2271
Db 2108 GCTTCAACATCAGCACAGCATCCGCGGCAAGGTGCAGAAAGGATACGCGCTTCTCTACA 2167
Qy 2272 GTCTGAGAGGCTAGCAGCTGCGACCCCTTACCGATTTTGACAGGGCTGGGGCCCTA 2331
Db 2168 AGTGGACATCATCCCATCGACAAACGACACACAGCTACAGCTGACAGCTGCAACA 2227
Qy 2332 TCAGTTATGCCAAGCGGCGCCGACAGCGCCCTACTCTGCTGGCACTACCCGCCA - 2390
Db 2228 CCAGCGTATCACCCAGGCTGCCCCAAGGTGAGCTTCGAGGCCATCCCCCAACCACTACT 2287
Qy 2391 --AAACCTTCCGTTATTTGTCGCGAGAGTGTGTGTCGCTGATTTATGCTTCACTC 2448
Db 2288 GCGCCCGCGCTTTCGCGATCTGAAAGTGCAGAGGACAAAGATTCAGCGGAAGGGCC 2347
Qy 2449 CCAGCGCGGTGTG---GTGGAAACGACGACAGGTGCGGGCGCGCCACCTACAGCTGG 2504
Db 2348 CTTGCAACCAAGTAGCAGCGTGCAGTGACCCACGCGATCCCGCCGCGGTGAGCACCC 2407
Qy 2505 GGTGAATAATGATACGAGCTTTCGTCTTAAACAATACAGGCGCACCGCTGGGCAATTGG 2564
Db 2408 AGCTGTCTGTAACGCTAGCTGCGCGAGGAGGTGGTGATCCCGCAGCGCTAACTTGG 2467
Qy 2565 TTGCTGTGATCTGGATGAATCACTGATGATTCACCAAGTGTGCGAGGGCT--CCTT 2622
Db 2468 CCGACAAACGCAAGGTGATCATCTGCGAGCTGAACGAGAGCGTGGAGATCAACTGCACCC 2527
Qy 2623 GTGTCTATCGGAGGGCGGCAACACACCTGCACTGCGCCACTGATTGCTTCGCAAGC 2682
Db 2528 GCCCAACAAACACCCGCAAGAGATTCACATCGCGCCCGCGCGCGGCTTCTACACCA 2587
Qy 2683 ATCCGACGCGCACATCTCTCGTGGGGCTCCGGTCCCTGGATCACACCCAGGTGCGTGG 2742
Db 2588 CCGCGCAGATCATCGCGACATCCGCGAGGCCCACTGCAACCTGAGCGCGCCCAAGTGA 2647
Qy 2743 TCAGCTACCGGTATAGCTTTGGATATTCCTTGTACATCAATACACCATATTTAAAA 2802
Db 2648 ACACACCTTGAACAAGATCTGTATCAAGTGGCGGAGAGTTTCGGCAACAAGACCATCG 2707
Qy 2803 TCAGGATGTACGTGGAGGGGTGMAACACAGGTGGAAGCTGCAACTGACGCGG 2862
Db 2708 TGTTCAGCAACAGCGCGCGGACCCCGAGATCTGTGACCCACAGCTTCACTGCGGCG 2767
Qy 2863 GCGAAGTTGCGATCTGGAAGATAGGACAGGTCCGAGATCGATATGGAGAAATCAACAT 2922
Db 2768 GCGAGTTCTTCTACTCAACAGCACCCAGCTGTTTCAACAGCACCTGTTTCAACAGCACCT 2827
Qy 2923 CAGGATTCAGACCCCTCTCTGTGTACAGCGGGGTTTTTCTGTTGACAAAGATCC 2982
Db 2828 GGAGCACCGAGGCGACAAAC-----ACCGAGGGCGAGCGACCATCACCCCTGCCCT 2881

Qy 2983 TCACAATACGCGAGCTCTAGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGAGTCTC 3042
Db 2882 GCGCATCAAGCAGATCATCAACATGTGGAGAAGTGGGCAAGCCATGTACGCCCCCC 2941
Qy 3043 CGGTGTCTTGGCCAAAATTTGCACTGCCAATCTCCCAATCACTCAACAACTCTCTGTC 3102
Db 2942 CCATCAGCGCCAGATCCGCTGAGCAGCAACATCACCGGCTCTGCTCAGCGCAGC 3001
Qy 3103 CTCCAATTTGCTCTGTTATCGCTGATGTCTGCGGGTTTTATCATATCTCTCTTCA 3162
Db 3002 GCGCAACAGCAACAAAGAGCGAGATCTTCCGTCCGGCGGGGCGGACATGCGCA 3061
Qy 3163 TCTGCTGTATATGCTCATCTTCTTATGTTTCTTCTGATATC---AAGTATGTTG 3218
Db 3062 ACTGCGCAGCGAGCTGTACAAGTCAAGTGTGGAAGTCAAGCCCTTGGCGTGGCCCC 3121
Qy 3219 CCGTTTGTCTTAATTCAGGATCAACAAACAGTACGGGACCATGCAAAACCTGTC 3278
Db 3122 CCACCAAGGCCAAGCTTACCGTCCAGGCCCGCAGCTGCTGAGCGGATCTGTCAGCAGC 3181
Qy 3279 ACGACTCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAT 3338
Db 3182 AGAACAACTGTGCGCGCATCGAGGCCAGCAGCACTGCTGCGAGCTGACCGTGTGGG 3241
Qy 3339 GGAATTTGCACTGTATTTCCCATCCCATCGTCTCTGG---GCTTTGCAAAATACCTATGG 3395
Db 3242 GCATCAAGCAGCTGCGAGCGCGCACCTTGGCGTGGAGCGCTACTGAGGACCGAGC 3301
Qy 3396 GAGTGGGCTCAGTCCGTTTCTTGGCTCAGTTTACTAGTGCCATTTGTTCAAGTGTTC 3455
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Job time : 2961 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 22:14:31 ; Search time 929 Seconds
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10360.150 Million cell updates/sec

Title: US-10-715-665-6

Perfect score: 5882

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4617.2	78.5	5459	4	US-09-721-480-4
3	4190	71.2	5128	4	US-09-721-480-2
4	2658.4	45.2	4276	4	US-09-721-480-1
5	2265.4	38.5	8575	5	PCT-US92-08258-6
6	2256.6	38.4	6565	3	US-09-299-141-1
7	2229.2	37.9	6280	3	US-08-893-327-19
8	2225.6	37.8	6280	3	US-08-893-327-17
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13	2166.4	36.8	4328	3	US-09-620-260-1
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ALIGNMENTS

RESULT 1

US-09-721-480-6

; Sequence 6, Application US/09721480

; Patent No. 6740323

; GENERAL INFORMATION:

; APPLICANT: Selby, Mark

; APPLICANT: Glazer, Edward

; APPLICANT: Houghton, Michael

; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE

; FILE REFERENCE: PP01635.002

; CURRENT APPLICATION NUMBER: US/09/721,480

; CURRENT FILING DATE: 2000-11-22

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 6

; LENGTH: 5882

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: plasmid

; OTHER INFORMATION: pCMV-II-E2661-sag

; NAME/KEY: CDS

; LOCATION: (1992)..(3584)

; US-09-721-480-6

Query Match 100.0%; Score 5882; DB 4; Length 5882;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5881 TC 5882
Db 5881 TC 5882
RESULT 2
US-09-721-480-4
; Sequence 4, Application US/09721480
; Patent No. 6740323
; GENERAL INFORMATION:
; APPLICANT: Selby, Mark
; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
; FILE REFERENCE: PPO1635.002
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5459
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pCMVII opti
; OTHER INFORMATION: 330 E1/Smg
; NAME/KEY: CDS
; LOCATION: (1992).. (3161)
US-09-721-480-4
Query Match 78.5%; Score 4617.2; DB 4; Length 5459;
Best Local Similarity 89.1%; Pred. No. 0; Mismatches 218; Indels 423; Gaps 7;
Matches 5241; Conservative 0;
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DB	2465	-----	2464
QY	2821	GGGTGAAACAAGGCTGGAAGCTGCTGCAATGAGCGGGGCGAAACGTTGCGATCTGG	2880
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QY	2941	TGCTCGTGTACAGGGGGGTTTTCTGTGACAGAAATCCTCAAAATACCGCAGAGTC	3000
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DB	2758	TCCTCTTATTTGGTTCTCTGGATTATCAAGGTATGTTGCCGTTTCTCTCTAAATCCAG	2817
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DB	3478	TGACTCGCTCGCTCGGTTCGCTCGGCGAGCGGTATCAGCTCATCTAAAAGCGGT	3537
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QY	4801	TGAGTAACTTGGTGTGACAGTTACAAATGCTTAATCAGTGGAGCACCTATCTCAGGAT	4860
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Qy 5881 TC 5882
Db 5458 TC 5459
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RESULT 3

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US-09-721-480-2
; Sequence 2, Application US/09721480
; Patent No. 6740323
; GENERAL INFORMATION:
; APPLICANT: Selby, Mark
; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
; FILE REFERENCE: PP01635.002
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; OTHER INFORMATION: pCMVII-ps2-sag
; NAME/KEY: CDS
; LOCATION: (1988)..(2830)
US-09-721-480-2
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Query Match 71.2%; Score 4190; DB 4; Length 5128;
Best Local Similarity 85.7%; Pred. No. 0;
Matches 5038; Conservative 0; Mismatches 90; Indels 754; Gaps 4;
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; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
; FILE REFERENCE: PP01635.002
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7

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; SOFTWARE: PatentIn Ver. 2.0  
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; TYPE: DNA  
; ORGANISM: Artificial Sequence  
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; OTHER INFORMATION: Description of Artificial Sequence: plasmid pCMVII  
US-09-721-480-1
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QY 781 GTATTAGTCAATCGCTATTACCATGGTGTGATGCGGTTTGGCAGTACACCAATGGCGGTGA 840  
Db 781 GTATTAGTCAATCGCTATTACCATGGTGTGATGCGGTTTGGCAGTACACCAATGGCGGTGA 840  
QY 841 TAGCGGTTTGAATCAGCGGGAATTTCCAGTCTCCACCCCAATGAGCTCAATGGGAGTTTG 900  
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901 TTTTGGCACCAGAAATCAACCGGACTTTTCCAAAATGCTGTAATAACCCCGCCCGTTGACG 960
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901 TTTTGGCACCAGAAATCAACCGGACTTTTCCAAAATGCTGTAATAACCCCGCCCGTTGACG 960
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961 CAAATGGCGGTAGGCGGTGACCGTGGGAGGTCTATATAGCAGAGCTCGTTTGTAGTAAC 1020
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961 CAAATGGCGGTAGGCGGTGACCGTGGGAGGTCTATATAGCAGAGCTCGTTTGTAGTAAC 1020
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1021 CGTCAGATCGCCTGGAGAGCCCATCAACGCTGTTTGTGACCTCCATAGAGACACCCGGAC 1080
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1081 CGATCAGCCTCCGCGCCGGGAAACCGTGCAATTTGGAAACGCGGATCCCGTGCCAAAGAT 1140
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1141 GAGCTAAGTACCCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCAATGCTATA 1200
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Db |||||
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1681 AGTGTCCGACACAGCCGCTGGCGGTAGGGTATGCTCTGAAATAGCTCGAGATTGG 1740
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1741 GCTCGCAGCTGGACGAGATGGAAGACTTTAAGCAGCGGAGAGAGATGAGGAGCT 1800
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1801 GAGTTGTTGTAATTCGATAGAGTACAGAGTAACTCCCGTTGCGGTGCTTTAAACGGTGG 1860
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1861 AGGGAGTGTAGTCTGAGCAGTACTGTTGCTGCGCGCGGCCACACAGATATAGCT 1920
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1921 GACAGACTAACAGACTGTTCTTTCCATGGGCTTTTTCGAGTACCGTCTGTCGACGAA 1980
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1981 TTCAAGCAATCATGGATGCAATGAAGAGGGGCTCTGCTGTGTGCTGCTGTGTGGAG 2040

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Qy |||||
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1978 ----- 1977
Qy |||||
2161 ACACCAACGCGAGTTGGCACCCTCAATAGCACGGCCCTGAACTGCAATGATAGCTCAACA 2220
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Qy |||||
2221 CCGGCTGTTGGCAGGCTTTTCTATCACCACAAAGTTCAACTCTTCAGGCTGTCCTGAGA 2280
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2281 GGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAGGCTGGGGCCCTATCAGTTATG 2340
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2341 CCAACGGAAGCGGCCCGGACCGCCCTACTGTGSGCACTACCCGCCAAAACCTTGGC 2400
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Qy |||||
2401 GTATTGTGCCCGGAAGAGTGTGTGTGTCGGTATATTGCTTCACTCCAGGCCCGCTGG 2460
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2641 GCAACAAACACCTGCACCTGCCACCTGATTGCTTCGCAAGCATCCGAGCGCCACATACT 2700
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Qy |||||
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Qy |||||
2821 CGGTGGAACACAGGCTGGAAGCTGCTCTCAACTGGACGCGGGCGGAAACGTTGCGATCTGG 2880
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2881 AAGATAGGACAGGTCCGAGATCGATATGGAACAATCATCATAGGATTCCTTAGGACCCC 2940
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2941 TGCTCGTGTACAGGGGGGTTTTTCTTGTGCAAGAAATCTCAACAATACCGCAGAGTC 3000
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3001 TAGACTCGTGGTGGACTCTCTCAATTTTCTAGGGGATCTCCCGTGTGTCTTTGGCCAAA 3060
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Qy 3241 GATCAACAACAACAGTACGGGACCATGCAAAACCTGCACGACTCCTGCTCAAGGCAACT 3300
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Qy 3301 CTATGTTTCCCTCATGTTGCTGTACAAACCTACCGGATGAAATTGCACCTGTATTTCCCA 3360
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Qy 3361 TCCCATGCTGGGTTTCGCAAAATACCTATGGAGTGGGCTCAGTCCGTTTCTCTT 3420
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Db 1978 ----- 1977
Qy 3481 TTTCAGCTATATGGATGTGTGTATTTGGGGGCCAAGTCTGTACAGCATGCTGAGTCCCT 3540
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Qy 3721 TCTTTGACCTGGAGGTGCCACTCCACTGCTTCTTCTTAAATGAGAAATTGCA 3780
Db 2115 TCTTTGACCTGGAGGTGCCACTCCACTGCTTCTTCTTAAATGAGAAATTGCA 2174
Qy 3781 TCGCATTTGTCTAGTAGTGTCTATTCTATTCTGGGGGGTGGGGTGGGGCAGACAGCAAG 3840
Db 2175 TGGCATTTGTCTGATGAGTGTCTATTCTATTCTGGGGGGTGGGGTGGGGCAGACAGCAAG 2234
Qy 3841 GGGGAGATTGGGAAGACAATAGCAGGCATGCTGGGGAGCTCTTCGCTTCTCGCTCAC 3900
Db 2235 GGGGAGATTGGGAAGACAATAGCAGGCATGCTGGGGAGCTCTTCGCTTCTCGCTCAC 2294
Qy 3901 TGACTCGCTCGCTCGCTTCTGGCTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT 3960
Db 2295 TGACTCGCTCGCTCGCTTCTGGCTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT 2354
Qy 3961 AATACGGTTATCCACAGAAATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCCA 4020
Db 2355 AATACGGTTATCCACAGAAATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCCA 2414
Qy 4021 GCAAAAGGCCAGGAACCGTAAAGCGCGTGTGCTGGGCTTTTCCATAGGCTCGGCC 4080
Db 2415 GCAAAAGGCCAGGAACCGTAAAGCGCGTGTGCTGGGCTTTTCCATAGGCTCGGCC 2474
Qy 4081 CCTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACT 4140
Db 2475 CCTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACT 2534
Qy 4141 ATAAAGATACAGGCGCTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTT 4200
Db 2535 ATAAAGATACAGGCGCTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTT 2594

Qy 4201 GCCGTTACCGGATACCTGTCTCGCCTTTCTCCCTCGGGAAGGTGGCCTTCTCAATG 4260
Db 2595 GCCGTTACCGGATACCTGTCTCGCCTTTCTCCCTCGGGAAGGTGGCCTTCTCAATG 2654
Qy 4261 CTCAGCGTGTAGGTATCTCAGTTCGCTGAGTTCGCTCCAGCTGGGCTGTGTGCA 4320
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Qy 4741 GATCTTCAGCTAGATCTTTTAAATTAAGATTTTAAATCAATCAATCAATCAATCAATCA 4800
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Qy 5161 GTCGTTTGTATGGCTTCAATTCAGTCCCGTTCCCAACCATCAAGCGGAGTTACATGATC 5220
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Qy 5221 CCCCATGTTGTCAAAAAAGCGGTTAGCTCTTTCGGTCTCCGATCGTTGTTCAGAGATTA 5280
Db 3615 CCCCATGTTGTCAAAAAAGCGGTTAGCTCTTTCGGTCTCCGATCGTTGTTCAGAGATTA 3674

5281	Qy	GTTTGGCCGAGTGTATTACATCATGTATTGGCGACACTGCATAAATCTCTTACTGTGCAT	5340
3675	Db	GTTTGGCCGAGTGTATTACATCATGTGTATTGGCAGCACTGCATAAATCTCTTACTGTGCAT	3734
5341	Qy	GCCATCCGTAAAGATGCTTTTCTGTGACTGTGTGAGTACTCAACCAAGATCAATCTCTGAGAAATA	5400
3735	Db	GCCATCCGTAAAGATGCTTTTCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTCTGAGAAATA	3794
5401	Qy	GTGTATGCGGCGACCGAGTTGCTCTTTGCCCGGGTCTCAATAACGGGATAAATACCGCGCCACA	5460
3795	Db	GTGTATGCGGCGACCGAGTTGCTCTTTGCCCGGGTCTCAATACGGGATAAATACCGCGCCACA	3854
5461	Qy	TACAGAACTTTAAAGTGTCTCATTTGAGTGAAGAACGTTCTTCGGGGCGGAAAATCTCTCAAG	5520
3855	Db	TACAGAACTTTAAAGTGTCTCATTTGAGTGAAGAACGTTCTTCGGGGCGGAAAATCTCTCAAG	3914
5521	Qy	GATCTTTACCGCTGTGTGAGATCCAGTTTCGATGTAAACCCACTCGTGACACCCAACTGATCTTC	5580
3915	Db	GATCTTTACCGCTGTGTGAGATCCAGTTTCGATGTAAACCCACTCGTGACACCCAACTGATCTTC	3974
5581	Qy	AGCATCTTTTACTTTTACACGAGGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCGCGC	5640
3975	Db	AGCATCTTTTACTTTTACACGAGGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCGCGC	4034
5641	Qy	AAAAAGGGAATAAGGCGGACACGGAAATCTTGAATACTCATACTCTTCCTCTTTTCAATA	5700
4035	Db	AAAAAGGGAATAAGGCGGACACGGAAATCTTGAATACTCATACTCTTCCTCTTTTCAATA	4094
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4095	Db	TTATTGAAGCAATTTATCAGGCGTTATTGTCTCATGACGGGATACATATTTGAATGTATTTTA	4154
5761	Qy	GAAAAATAAACAAATAGGGGTTTCGGCGCACATTTCCCGAAAAAGTGCCACCTGACGCTCTA	5820
4155	Db	GAAAAATAAACAAATAGGGGTTTCGGCGCACATTTCCCGAAAAAGTGCCACCTGACGCTCTA	4214
5821	Qy	AGAAACCATATTATTATCATGACATTTAAACCTATAAAAAATAGGCGGTATCACGAGGCGCTTTTCG	5880
4215	Db	AGAAACCATATTATTATCATGACATTTAAACCTATAAAAAATAGGCGGTATCACGAGGCGCTTTTCG	4274
5881	Qy	TC 5882	
4275	Db	TC 4276	

RESULT 5
 PCT-US92-08258-6
 ; Sequence 6, Application PC/TUS9208258
 ; GENERAL INFORMATION:
 ; APPLICANT: GENENTECH, INC. and STATE OF OREGON BY AND
 ; TITLE OF INVENTION: PRODUCTION OF GPA NEUROTROPIC FACTOR
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 940804990
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/08258
 ; FILING DATE: 19920929
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Johnston, Sean A.

QY 1275 GGGTTATTGACCAATTATTGACCACTCCCTAT-----TGGTGAGGATACTTTCC 1323
Db 3887 GCCTTTCTCTCCACAGGTGTCACTCCCAAGTCCAACTGCACCTCGGTCTATTCGATTGG 3946
QY 1324 ATTACTAATCCATAACATGGCTCTTTGGCCACAACATATCTCTATTGGCTATATGCCAATAC 1383
Db 3947 CCTTGGTGGCCAGCTGAGCTCACTCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 4006
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Db 4427 TTTCACAAATAAAGCAATTTTCTACTGCAATCTAGTTGGTTTGTCCAAACTCATCA 4486
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Db 4487 TGTATCTTATCATGCTCGATCGGGAATTAATTCGGGCGGCGAGTCTGACCTGCACCCA 4546
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QY 2044 TCTTCG---TTTCGCCAGCGCTAGCGAAACCCACGTCACCGGGGAAAGTGGCGGCCA 2100
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Db 5557 GCAGTACGGTGTGCTCCATCAGTTTGCAGTGTATACATGGGATCAGCAATCGCG 5616
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Db 5737 AGAACAGCGGGCAGTTCCGTTTTCAGCAGGCTCTTGCAAGTGCACCTGTGCACGGCG 5796
QY 3159 TTCACTCTGCTGATGCTCTCATCTTCTTATTGTTCTTCTGGAATTCAGAGTATGTTG 3218
Db 5797 GAGATCAATAGGTGAGGCTCTCGCTGAATTTCCCAATGTCAAGCACTTCGCGAATCGGG 5856
QY 3219 CCGTTTGTCTTAATTCAGGATCAACAAACAGTACGGGACCATGCAAAACCTGC 3278
Db 5857 AGCGGGCCGATGCAAGTGGCGATAAC-ATAACGATCTTTGTAGAAACCATCGGCGCA 5915
QY 3279 ACGACTCTCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGTGTGTACAA-----AACC 3331
Db 5916 GCTATTTATCCCGCAGGACATATCCACGCCCTCTCATATCGAAAGTGAAGCAGCATTC 5975
QY 3332 TAGGATGAATAATGCACTGTATTTCCCATCCATCGCTCGTGGCTTTTCGCAAAATACCT 3391
Db 5976 TTCGCCCTCCGAGAGTGCATCAGGTCCGAGACGCTGTGCAACTTTTTCGATCAGAACTT 6035
QY 3392 ATGGGAGTGGGCTCAGTCCGTTTCTTCTTGGCTCAGTTTACTAGTGCCATTTTGTTCAGTG 3451

Db 6036 CTGACAGACGTCGCGGTGAGTTTCAGGCTTTTTCATATCTCAATTGCCCCGAGCAGGGA 6095
Qy 3452 GTTCGTAGGGCTTCCCCACTGTTTGGCTTTCAGCTATATGATGATGTTGTTGAGG 3511
Db 6096 TCTGCGGCACGCTGTGTACGCTGTAAAGCGGGTCGTCGAGGGTCGCTCGGTGTTCAGG 6155
Qy 3512 GCCAAGTCTGTACAGCATCGTGAGT-----CCCTTTATPACCGCTGTGTACCAATTTCTCTTT 3567
Db 6156 CCACACGCGTCACTTAATATGCGAAGTGGAACCTCGGACCGCGCCCGGACTGCACT 6215
Qy 3568 GTCTCTGGGTATACATTTAAGAAATTCAGACT-----CGAGCAAGTCTAGAAAGGCGCGC 3621
Db 6216 GCGTGTTCGAATTCGCGCAATGCAACAGACGCTGGCGGGGTTTGTGTCAATCATAGAACTAA 6275
Qy 3622 CAAGATATCAAGGATCACTACGCTTACGCTTACGCTGCTGATCAGCTCGACTGTCCTTCT 3681
Db 6276 AGCATGCAATATATTTCTTCGCGGGACACCGCCAGCAACGCGAGCAACGGGCGACCG 6335
Qy 3682 AGTTG--CCAGCCATCTGTTGTTTGGCCCTCCCGCTGCTTCCCTTGACCCCTGGAAGGTG 3739
Db 6336 GGATGAAGCAGGCGACGCTCTGGTCAATTTTCGGCGAGGACCGCTTTCGCTGGAGGCG 6395
Qy 3740 CCACTCCCATGCTCTTCTTAATAAAATGAGAAATTTGCATCGCATTTGCTGAGTAGGT 3799
Db 6396 ACCATGATCGGCCCTGCTGCTTGGGTATTCGGAATCTTGACGCCCTCGCTCAAGCCTTC 6455
Qy 3800 GTCATTTCTATCTTGGGGGTGGGTGGGCGAGCAGCAGCAAGGGGAGGATTTGGAGACA 3859
Db 6456 GTCACTGGTCCCGCCACCAAAAGTTTCGGCGAAGCAGGCGCATATATCGCGCGCATGGCG 6515
Qy 3860 ATAGCAGGCACTGTGGGAGCTCTTCGCTTCTCGCTCACTGACTCGCTCGCTCGGTG 3919
Db 6516 GCCGACGCGTGGCTACGCTTCTGCTGGCTTCGCGACGCGAGGCTGGATGGCTTCCCC 6575
Qy 3920 GTTCGCGTGGCGGAGCGGTATCAGCTCACTCAAAAGCGGTATACGGTTATCCACAGAA 3979
Db 6576 ATTATGATTTCTTCGCTTCGCGGCATCGCGATGCCCCGTTTCAGGCGCATGCTGTCC 6635
Qy 3980 TCAGGGGATACCGGAGAAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGACCGT 4039
Db 6636 AGCGCATAGATACCAACCATCAGGAGACAGCTAAAAGGCGCAGCAAAAGGCCAGGACCGT 6695
Qy 4040 AAAAGGCCCGCTGTGCTGGCGTTTTCATAGGCTCCGCCCTCCCTGACAGCATCACAA 4099
Db 6696 AAAAGGCCCGCTGTGCTGGCGTTTTCATAGGCTTCGCGCTCCGCTGACGAGCATCACAA 6755
Qy 4100 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCGAGCGTT 4159
Db 6756 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCGAGCGTT 6815
Qy 4160 CCCCCTGGAGCTCCCTCGTGGCTCTCCTGTTCCGACCTCGCGCTTACCGGATACCTG 4219
Db 6816 CCCCCTGGAGCTCCCTCGTGGCTCTCCTGTTCCGACCTCGCGCTTACCGGATACCTG 6875
Qy 4220 TCCGCTCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTC 4279
Db 6876 TCCGCTCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTC 6935
Qy 4280 AGTTCCGCTGAGTGTGCTTCCCTCAAGCTGGGTGTGTGCAACCCCGCTTACGCC 4339
Db 6936 AGTTCCGCTGAGTGTGCTTCCCTCAAGCTGGGTGTGTGCAACCCCGCTTACGCC 6995
Qy 4340 GACCGCTGGCTTATCCGCTATCTATCTGTTAGTCCACCCGCTTACGACGACTTA 4399
Db 6996 GACCGCTGGCTTATCCGCTATCTATCTGTTAGTCCACCCGCTTACGACGACTTA 7055
Qy 4400 TCCGCTGACGACGACCTGGTAAACAGGATTTAGCAGGAGGATGTAGCGGTGCT 4459
Db 7056 TCCGCTGACGACGACCTGGTAAACAGGATTTAGCAGGAGGATGTAGCGGTGCT 7115
Qy 4460 ACAGAGTCTTGAAGTGGTGGCTTAACCTAGCGCTACACTAGAAAGGACAGTATTTGGTATC 4519

Db 7116 ACAGAGTCTTGAAGTGGTGGCTTAACCTAGCGCTACACTAGAAAGGACAGTATTTGGTATC 7175
Qy 4520 TCGGCTCTGCTGAAGCAGGTTACTTCGGAAAAAGAGTTGGTAGCTCTTCATCCGCAAA 4579
Db 7176 TCGGCTCTGCTGAAGCAGGTTACTTCGGAAAAAGAGTTGGTAGCTCTTCATCCGCAAA 7235
Qy 4580 CAAACACACGCTGGTGAAGCGTGGTTTTTTTGTGCAAGCAGCAGATTTACGCGCAGAAAA 4639
Db 7236 CAAACACACGCTGGTGAAGCGTGGTTTTTTTGTGCAAGCAGCAGATTTACGCGCAGAAAA 7295
Qy 4640 AAGGATCTCAAGAAAGATCTTTTGTATCTTTTCTAGCGGCTCTGACGCTCAGTGAAGAA 4699
Db 7296 AAGGATCTCAAGAAAGATCTTTTGTATCTTTTCTAGCGGCTCTGACGCTCAGTGAAGAA 7355
Qy 4700 AACTCAGCTTAAGGATTTTGGTCATGAGATATCAAAAAGGATCTTCACTAGATCTTT 4759
Db 7356 AACTCAGCTTAAGGATTTTGGTCATGAGATATCAAAAAGGATCTTCACTAGATCTTT 7415
Qy 4760 TTAATTTAAAAATGAAGTTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGAC 4819
Db 7416 TTAATTTAAAAATGAAGTTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGAC 7475
Qy 4820 AGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGGATCTGTCTATTTCTGTTATCC 4879
Db 7476 AGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGGATCTGTCTATTTCTGTTATCC 7535
Qy 4880 ATAGTTGCTGACTCCCGTCTGTAGATAACTACGATACGGGAGGCTTACCATCTGGC 4939
Db 7536 ATAGTTGCTGACTCCCGTCTGTAGATAACTACGATACGGGAGGCTTACCATCTGGC 7595
Qy 4940 CCAGTGTCTGCAATGATACCGGAGACCCACGCTCACCAGCTCCAGATTTATCAGCAATA 4999
Db 7596 CCAGTGTCTGCAATGATACCGGAGACCCACGCTCACCAGCTCCAGATTTATCAGCAATA 7655
Qy 5000 AACCGCAGCGCGAAAGGCGCGAGCGCAGAGTGTCTGCAACTTTATCCGCTCCATC 5059
Db 7656 AACCGCAGCGCGAAAGGCGCGAGCGCAGAGTGTCTGCAACTTTATCCGCTCCATC 7715
Qy 5060 CAGTCTATTAAATTTGTTCGGGAAGCTAGAGTAAAGTAGTTTCGCGAGTTAATAGTTTGGC 5119
Db 7716 CAGTCTATTAAATTTGTTCGGGAAGCTAGAGTAAAGTAGTTTCGCGAGTTAATAGTTTGGC 7775
Qy 5120 AACGTTGTTGCCATTTGCTACAGGCACTCGTGTGTCTACGCTCGTGTGTTGGTATGGCTTCA 5179
Db 7776 AACGTTGTTGCCATTTGCTACAGGCACTCGTGTGTCTACGCTCGTGTGTTGGTATGGCTTCA 7835
Qy 5180 TTCAGCTCCGTTTCCCAACGATCAAGCGAGTTAATGATGCCCATGTTGTGCAAAAAA 5239
Db 7836 TTCAGCTCCGTTTCCCAACGATCAAGCGAGTTAATGATGCCCATGTTGTGCAAAAAA 7895
Qy 5240 GCGGTTAGCTCTTCGGTCTCCGATCGTTGTGCAAGTAAAGTTGCGCGCAGTGTATCA 5299
Db 7896 GCGGTTAGCTCTTCGGTCTCCGATCGTTGTGCAAGTAAAGTTGCGCGCAGTGTATCA 7955
Qy 5300 CTCATGTTTATGGCAGCACTGCATAATTTCTTACTGTCTATGCCATCCGTAAGATGCTTT 5359
Db 7956 CTCATGTTTATGGCAGCACTGCATAATTTCTTACTGTCTATGCCATCCGTAAGATGCTTT 8015
Qy 5360 TCTGTGACTGGTGAAGTACTCAACCAAGTCAATCTCGAGAAATAGTGTATGCGGCGACCGAGT 5419
Db 8016 TCTGTGACTGGTGAAGTACTCAACCAAGTCAATCTCGAGAAATAGTGTATGCGGCGACCGAGT 8075
Qy 5420 TCGCTCTGCGCGCTCAATACGGGATATACCGCGCATATACCGCGCATAGCAGAACTTTAAAGTG 5479
Db 8076 TCGCTCTGCGCGCTCAACACGGGATATACCGCGCATATACCGCGCATAGCAGAACTTTAAAGTG 8135
Qy 5480 CTCATCATTTGGAAGAGCTTTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGA 5539
Db 8136 CTCATCATTTGGAAGAGCTTTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGA 8195
Qy 5540 TCCAGTTCGATGTAAACCCACTCGTGCAACCAACTGATCTTTCAGCATCTTTTACTTTCAAC 5599
Db 8196 TCCAGTTCGATGTAAACCCACTCGTGCAACCAACTGATCTTTCAGCATCTTTTACTTTCAAC 8255

QY 5600 AGCGTTTCGGGTGACGCAAAACAGGAAGCAGAAATGCCGCAAAAAGGGAATAAGGGCG 5659
DB 8256 AGCGTTTCGGGTGACGCAAAACAGGAAGCAGAAATGCCGCAAAAAGGGAATAAGGGCG 8315
QY 5660 ACACGGAATGTTGAATACCTCATACTCTCTCTTTTCAATATTATTGAAGCATTATATCAG 5719
DB 8316 ACACGGAATGTTGAATACCTCATACTCTCTCTTTTCAATATTATTGAAGCATTATATCAG 8375
QY 5720 GGTATTGTCTCATGACGGATACATATTGTAATGTATTAGAAAAATAAACAATPAGG 5779
DB 8376 GGTATTGTCTCATGACGGATACATATTGTAATGTATTAGAAAAATAAACAATPAGG 8435
QY 5780 GTTCCGCGACATTTCCCGGAAAGTGCACCTGACGTCTAGAAACCAATTATTATCATG 5839
DB 8436 GTTCCGCGACATTTCCCGGAAAGTGCACCTGACGTCTAGAAACCAATTATTATCATG 8495
QY 5840 ACATTAACTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC 5882
DB 8496 ACATTAACTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC 8538

RESULT 6
US-09-299-141-1
; Sequence 1, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6565
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PLASMID C-AT
US-09-299-141-1

Query Match 38.4%; Score 2256.6; DB 3; Length 6565;
Best Local Similarity 65.2%; Pred. No. 0;
Matches 3676; Conservative 0; Mismatches 1689; Indels 276; Gaps 13;

QY 495 GTTCCGCGTTACATAACTTACGGTAAATGGCCGCTGGCTGACCGCCCAACGACCCCG 554
DB 176 GTTACCGGTTACATACTTACGGTAAATGGCCGCTGGCTGACCGCCCAACGACCCCG 235
QY 555 CCCATTGACGTCNATTAATGACGTATGTTCCCATAGTAAGCCCATAGGACCTTCCATTG 614
DB 236 CCCATTGACGTCNATTAATGACGTATGTTCCCATAGTAAGCCCATAGGACCTTCCATTG 295
QY 615 ACCTCAATGGGTGGAGTATTACGGTAAATGCCCACTTGGCAGTACATCAAGTGTATCA 674
DB 296 AGTCNATGGGTGGAGTATTACGGTAAATGCCCACTTGGCAGTACATCAAGTGTATCA 355
QY 675 TATGCCAAGTCGCGCCCTATTGACGTCAATGACGTAAATGGCCCGCTGGCATTTATGC 734
DB 356 TATGCCAAGTCGCGCCCTATTGACGTCAATGACGTAAATGGCCCGCTGGCATTTATGC 415
QY 735 CCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCACTAGTATTAGTATCGC 794
DB 416 CCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCACTAGTATTAGTATCGC 475
QY 795 TATTACCATGGTGATCGGTTTTGGCAGTACACCAATGGCGGTGGATAGCGGTTTGACTC 854

DB 476 TATTACCATGGTGATCGGTTTTGGCAGTACATCAATGGCGGTGGATAGCGGTTTGACTC 535
QY 855 ACGGGGATTTCAAAGTCTCACCCTATTCAGCGTCAATGGGAGTTTGTGTTTGGCACCAGAAA 914
DB 536 ACGGGGATTTCAAAGTCTCACCCTATTCAGCGTCAATGGGAGTTTGTGTTTGGCACCAGAAA 595
QY 915 TCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCCCGTTGACGCAAAATGGGCGGTAG 974
DB 596 TCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCCCGTTGACGCAAAATGGGCGGTAG 655
QY 975 GCGGTACCGGTGGGAGGTCTATATAAGCAGAGCTCGTTTTAGTGAACCGTCAGATCCGCTG 1034
DB 656 GCGGTACCGGTGGGAGGTCTATATAAGCAGAGCTCGTTTTAGTGAACCGTCAGATCCGCTG 715
QY 1035 GAGACCGCATCAACGCTGTTTTGACCTCCATAGAAGACACCGGACCGATCCAGCCTCCG 1094
DB 716 GAGACCGCATCAACGCTGTTTTGACCTCCATAGAAGACACCGGACCGATCCAGCCTCCG 775
QY 1095 CGGCCGGGAACGGTGCAATTGGAAACGGGATTCGCCGTGCCAAGAGTGAGTAAGTACCGC 1154
DB 776 GACTCTAGAACTAGTGGATCCC CGGGCTG CAGGAATTCGATATCAAGCTTGGGGATTTT 835
QY 1155 CTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCATGTCTATCTGTTTTTGGCTTG 1214
DB 836 CAGGCACACCACTGACCTGGGACAGTGAATCGACATGCCGCTCTCTGCTCGTGGGCG 895
QY 1215 GGGCTATACACCCCGCTCTTATGCTATAGGTGATGTTAGCTTATAGGTTGTT 1274
DB 896 ATCCTCTGCTGGCAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
QY 1275 GGGTTATTGACCATTTATGACCACCTCCCTATTTGGTGACGATACTTTCCATTACTAATCC 1334
DB 956 GGAGATGCTGCCAAGAACAGACATATCCACCATGATCAGGATCACCAACCTTCAAC 1015
QY 1335 ATAACATGGCTCTTTGGCCACAACTATCTCTATTGGCTATATGCCAATACTCTGCTCCTTCA 1394
DB 1016 AAGATCACCCCAACCTGGCTGAGTTGCGCTTACGCTATACCGCAGCTGGCACACCAG 1075
QY 1395 GAGACTGACACGGACTCTGTATTTTTTACAGGATGGGCTCCATTTATATTATTAACA--ATT 1452
DB 1076 TCCAACAGCACCAATATCTTCTCTCCCACTGAGCATCGCTACAGCCTTTGCAATGCTC 1135
QY 1453 CACATATACAAACGCGCTCCCGTCCCGCAGTTTTTTTATTAACATAGCGTGGGATC 1512
DB 1136 TCCCTGGGACCAAGGCTGACACTCAGATGAAATCCTGGAGGCTGAAATTTCAACCTC 1195
QY 1513 TCCGACATCTCGGTAACGTGTTCCGGACATGGGCTCTTCTCCGGTAGCGCGGAGCTTCC 1572
DB 1196 ACGGAGATTCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACCTCCTCGTACCCCTCAAC 1255
QY 1573 ACATCGAGCCCTGGTCCCATCCGTCACGCGGCTCATGTGCTGGCAGCTCCTGTTGCTC 1632
DB 1256 CAGCCAGACAGCAGCTCCAGCTGACCAACCGCAATGGCTGTTCTCTCAGCGAGGCGCTG 1315
QY 1633 CTAAACAGTGGAGCCAGACTTAGGCACAGCAAAATGCCCAACCAACCAAGTGTGCCGCAC 1692
DB 1316 AAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAGTTGTACACTCAGAAGCCTTCACT 1375
QY 1693 AAGGCGCTGGCGGTAGGTTATGTCTGAAAATGAGCTCGGAGATTGGGCTCGACCTGG 1752
DB 1376 GTCMACTTCGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTCAGTGGAGAAGGT 1435
QY 1753 AGCAGATGGAAGACTTAAAGGACGGGAGAGAGAGATCAGGACCTCAGTGTGTTGTAT 1812
DB 1436 ACTC--AAGGAAAAATTTGGGATTTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTTGCTC 1493
QY 1813 TCTGATAACAGTCAGAGGTAACTCCCGTTGCGTGTGTTAAACGGTGGAGGCGAGTGTAG 1872
DB 1494 TGGTGAATTACATCTTCTTTTAAAGGCAATGGG---AGAGACCTTTGAAGTCAAGGACA 1550
QY 1873 TCTGAGCAGTACTCTGTTGCTGCCGCGCGCCACCAAGACATTAATAGCTGACAGACTAACA 1932
DB 1551 CCGAGGAAGAGGACTTCCACGTTGGACCGGTCACCAACCGGTGACCCCGTGAAGTGCCTATGATGAAGC 1610

QY	1933	GACTGTTCTCTTTCATNGGGTCTTTTCTGCACTCAACGTCGTCGACGAATTCACAGCAATCA	1992
DB	1611	GTTTAGGCATGTTTAAATCATCCAGCACTGTAAAGAACTGTTCAGCTGGGTGCTGCTGATGA	1670
QY	1993	TGGATGCAAATGAAGAGAGGGCTCGCTGTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTGTT	2052
DB	1671	AATACCTGGGGCAATGCCACGCCCATCTTCTTCCTGCTGTATGAGGGGAAATACAGCAACC	1730
QY	2053	CGCCAGCGCTAGCGAAACCCACGTCACCGGGGGAAGTCGCGGCCACACATGTGTCTGAT	2112
DB	1731	TGGAAATGAACTCACCCAGATATCATCCAAAGTTCTTGGAAATGAAGACAGAGGT	1790
QY	2113	TTGTTAGCTCTCGCACCC---AGGCGCAAGACGAAAGCTTCAGCTGATCAACACCAACG	2169
DB	1791	CTGCCAGCTTACATTTATCCCAAACTGTCCATTAATCGAAACCTATGATCTGAAGAGCGTCC	1850
QY	2170	GCAGTGGCACCTCAATAGACAGCGCCCTGAACTGCAATGATAGCTCAACACCGGCTGGT	2229
DB	1851	TGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCAAG	1910
QY	2230	TGGCAGGGCTTTTCTATCACCAAGTTCAACTCTTCAGGCTGTCTTCAGAGGCTAGCCA	2289
DB	1911	AGGAGGCACCCCTGAAGCTCTCCAAAGCCGTG-CATTAAGGCTGTGTGACCATGACGAG	1969
QY	2290	GCTGCCGACCCCTTACCGATTTTGACAGGGCTGGGCCCTTACGATTATGCCAAACGAA	2349
DB	1970	AAAGGACTGAAGCTGTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCTCCCCC	2029
QY	2350	GGCGCCCGACAGCGGCCCTTACTGTGTGCACACTACCCCCAAAACCTTGGGGTATTTGTGC	2409
DB	2030	GAGTCAAGTTCAACAAACCCCTTTGTCTTTAATGATTGAACAAAATACCAAGTCTCCC	2089
QY	2410	CCGGAAGAGTGTGTGGTCCGGTATATTGCTTCACTCCAGCCCGTGGTGGGAA	2469
DB	2090	CTCTTCATGGGAAAGTGGTGAATCCCAACCAAAATAACTGCGCTCTCCTCAACCC	2149
QY	2470	CGACCGACAGTCCGGGCGGCCACCTACAGCTGGGGTGAAAAATGATACGGACGTCTTCG	2529
DB	2150	CTCCCTCCATCCTCGGCCCTCCCTGGATGACATTTAAAGAGGGTTGAGCTGGTAACC	2209
QY	2530	TCCTTAACAATACAGGCGCACCGCTGGGCAATTGGTTCCGTTGTACTCTGATGAATCAA	2589
DB	2210	CCCCCCCCCTCGCAGGGGCCCTCGAGCAGTGTGGTTTTTTCGAAGAGGAACAAAAGCCT	2269
QY	2590	CTGGATTACCAAAAGTGTGGAGCGCC-----TCCTGTGTCACTCGAGAGGGCG	2639
DB	2270	CTCACCCAGGCTGGAAATGTTTCCACCAGTGAAGGCAAGTGTGGTTTTCGAAGGGA	2329
QY	2640	GGCAACAACACCTCGACTGCCCCACCTGATTGCTTCGCAAGCATCCGACGCAATAC	2699
DB	2330	AGCAAAAGCCCTCCACCCAGGCCCTGGAATGTTTCCACCAATGTGCGACCAACC---C	2386
QY	2700	TCTCGGTGGGCTCCGGTCCCTGTGATCACACCGAGTGCCTGTGTCGACTACCCGTAAGG	2759
DB	2387	GCCCAGGCTCTTGTTCATTGGCGAATTCGAACACGCAATGCGAGTCCGGGGCGGCTCC	2446
QY	2760	CTTTGGCATATCTCTGTACCATCACTACACCATATTTAAATCAGGATGTAGTGGGA	2819
DB	2447	CAGTCCACTTCGATATTAAGTGTGACGCGTGTGGCCCTCGAACAACGAGGACCCCTGCAG	2506
QY	2820	GGGCTCGAAACACAGGCTTGGAAAGCTGCTCGCAACTGGACCGGGGCGAACTTTCGATCTG	2879
DB	2507	CCAATATGGGATCGGCCATTGAAACAAGTGAATGTCACGCAAGTTCCTCCGGCCGCTTGG	2566
QY	2880	GAAGATAGGACAGGTCGAGATCGATATGGAGAACATCATCAGAGATTCTTAGGACCC	2939
DB	2567	TGGAGAGGCTATTCCGGCTATGACTGGGCAACAACAGACAATCGGCTGCTCTGATGCGCGC	2626
QY	2940	CTGCTCGTGTACAGGCGGGTTTTCTTGTGTGACAGAAATCTTCACAAATACCGCAGAT	2999
DB	2627	TGTTCCGGCTGTACGCGAGCGGGCGCCGGTT-----CTTTTGTTCAGACCAACCTGT	2680

[illegible]

Db	3753	GGCCAAACGCGGGGAGAGCGGTTTGGTATTTGGGCGCTCTTCCGCTCTCCGCTCACT	3812
QY	3902	GACTCGCTGGCTTCGGTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTA	3961
Db	3813	GACTCGCTGGCTTCGGTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTA	3872
QY	3962	ATACGGTTATCCACAGAAATCAGGGGATACGCGAGGAAGAAATGTGAGCAAAAGCCAG	4021
Db	3873	ATACGGTTATCCACAGAAATCAGGGGATACGCGAGGAAGAAATGTGAGCAAAAGCCAG	3932
QY	4022	CRAAGCCAGGAACCGTAAAAAGGCCGCTTCGCTCGCGCTTTTCCATAGGCTCCGCC	4081
Db	3933	CRAAGCCAGGAACCGTAAAAAGGCCGCTTCGCTCGCGCTTTTCCATAGGCTCCGCC	3992
QY	4082	CCTGACGAGCATCAAAAAATCAGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGACTA	4141
Db	3993	CCTGACGAGCATCAAAAAATCAGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGACTA	4052
QY	4142	TAAAGATACAGGCGTTTCCCTCGGAAGTCCCTCGTGGCTCTCCTGTTCGACCCCTG	4201
Db	4053	TAAAGATACAGGCGTTTCCCTCGGAAGTCCCTCGTGGCTCTCCTGTTCGACCCCTG	4112
QY	4202	CGCTTTACCGGATACCTGTCGGCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGC	4261
Db	4113	CGCTTTACCGGATACCTGTCGGCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGC	4172
QY	4262	TCACGCTGTAGGTATCTCAGTTCGGTGTAGTGTTCGCTTCCAAAGTCGGCTGTGTGCAC	4321
Db	4173	TCACGCTGTAGGTATCTCAGTTCGGTGTAGTGTTCGCTTCCAAAGTCGGCTGTGTGCAC	4232
QY	4322	GAACCCCGCTTCAGCCGACCGCTGCTTATCCGGTAACTATCGTCTTGAGTCCAAC	4381
Db	4233	GAACCCCGCTTCAGCCGACCGCTGCTTATCCGGTAACTATCGTCTTGAGTCCAAC	4292
QY	4382	CCGCTAAGACACCACTTATCCGCACTGGCAGAGCCACTGGTAACAGGATTAGCAGCG	4441
Db	4293	CCGCTAAGACACCACTTATCCGCACTGGCAGAGCCACTGGTAACAGGATTAGCAGCG	4352
QY	4442	AGGTATGTAGCGGTGCTACAGAGTCTTTGAAGTGTGGCTAACTACGGCTACACTAGA	4501
Db	4353	AGGTATGTAGCGGTGCTACAGAGTCTTTGAAGTGTGGCTAACTACGGCTACACTAGA	4412
QY	4502	AGGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGT	4561
Db	4413	AGGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGT	4472
QY	4562	AGCTCTTGATCCGGCAAAACAAACACCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT	4621
Db	4473	AGCTCTTGATCCGGCAAAACAAACACCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT	4532
QY	4622	CAGATTACGGCGAGAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGGTCT	4681
Db	4533	CAGATTACGGCGAGAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGGTCT	4592
QY	4682	GACGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTTGGTCAAGATTTATCAAAAAG	4741
Db	4593	GACGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTTGGTCAAGATTTATCAAAAAG	4652
QY	4742	ATCTTCACCTAGATCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATAT	4801
Db	4653	ATCTTCACCTAGATCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATAT	4712
QY	4802	GAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATC	4861
Db	4713	GAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATC	4772
QY	4862	TGCTATTTGCTTCATCCATAGTTGGCTGACTCCCGCTGGTGGTGGTGGTGGTGGTGGT	4921
Db	4773	TGCTATTTGCTTCATCCATAGTTGGCTGACTCCCGCTGGTGGTGGTGGTGGTGGTGGT	4832
QY	4922	GAGGGCTTACCATCTGGCCCCAGTGTGCAATACCGGAGACCCACGCTCACCAGCT	4981

Db	4833	GAGGGCTTACCATCTGGCCCCAGTGTGCAATGATATACCGGAGACCCACGCTCACGGCT	4892
QY	4982	CCAGATTTATCAGCAATAAACACAGCAGCCGGAAGGCCGCGAGCGCAAGAGTGGTCTTGA	5041
Db	4893	CCAGATTTATCAGCAATAAACACAGCAGCCGGAAGGCCGCGAGCGCAAGAGTGGTCTTGA	4952
QY	5042	ACTTTATCCGCTCCATCCAGTCTATTATTTGTTGCCGGAAGCTAGAGTAAGTGTTCG	5101
Db	4953	ACTTTATCCGCTCCATCCAGTCTATTATTTGTTGCCGGAAGCTAGAGTAAGTGTTCG	5012
QY	5102	CCAGTTAATAGTTTGGCAACGTTGTCATTTGCTACAGGCATCGTGTGTCAACGCTCG	5161
Db	5013	CCAGTTAATAGTTTGGCAACGTTGTCATTTGCTACAGGCATCGTGTGTCAACGCTCG	5072
QY	5162	TCGTTTGGTATGGCTTCATTCAGTCCGCTTCCAAACGATCAAGCGAGTTACATGATCC	5221
Db	5073	TCGTTTGGTATGGCTTCATTCAGTCCGCTTCCAAACGATCAAGCGAGTTACATGATCC	5132
QY	5222	CCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTCTCAGAACTAG	5281
Db	5133	CCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTCTCAGAACTAG	5192
QY	5282	TTGGCCGCGAGTGTATCACTCATGTGTTATGGCAGCACTGCATAAATCTCTTACTGTCA	5341
Db	5193	TTGGCCGCGAGTGTATCACTCATGTGTTATGGCAGCACTGCATAAATCTCTTACTGTCA	5252
QY	5342	CCATCCGTAAAGTGTCTTCTGTGACTGTGTGATCTCAACCAAGTCACTCTGAGAAATAG	5401
Db	5253	CCATCCGTAAAGTGTCTTCTGTGACTGTGTGATCTCAACCAAGTCACTCTGAGAAATAG	5312
QY	5402	TCGTATCCGCGACCGAGTGTCTTTCGCGCGGTCAATAACGGGATAATACCGCGCCACAT	5461
Db	5313	TCGTATCCGCGACCGAGTGTCTTTCGCGCGGTCAATAACGGGATAATACCGCGCCACAT	5372
QY	5462	AGCAGAACTTTAAAAGTGTCTCATTTGAAAAACGTTCTTCGGGGCGAAAACTCTCAAGG	5521
Db	5373	AGCAGAACTTTAAAAGTGTCTCATTTGAAAAACGTTCTTCGGGGCGAAAACTCTCAAGG	5432
QY	5522	ATCTTACCGCTGTGTGAGATCCAGTTCGATGTAAACCCACTCTGTGCAACCACTGATCTTCA	5581
Db	5433	ATCTTACCGCTGTGTGAGATCCAGTTCGATGTAAACCCACTCTGTGCAACCACTGATCTTCA	5492
QY	5582	GCATCTTTTACTTTCACAGCGTTCCTGGTGCAGCAAAACAGGAGGCAAAATGCCGA	5641
Db	5493	GCATCTTTTACTTTCACAGCGTTCCTGGTGCAGCAAAACAGGAGGCAAAATGCCGA	5552
QY	5642	AAAAAGGGAATAAGGGCGCACACGAAATGTTGAATACTCATACTCTCTCTTTTCAATAT	5701
Db	5553	AAAAAGGGAATAAGGGCGCACACGAAATGTTGAATACTCATACTCTCTCTTTTCAATAT	5612
QY	5702	TATTTGAAGCATTTATCAGGGTTATTTGTCATGAGCGGATACATATTTGAATGATTTAG	5761
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QY	5762	AAAAATAACAATAAGGGGTTCCGGCGACATTTCCCGAAAAAGTGCCACTGACGCTTAA	5821
Db	5673	AAAAATAACAATAAGGGGTTCCGGCGACATTTCCCGAAAAAGTGCCACTGACGCTTAA	5732
QY	5822	GAAACCATTTATCATGACATTAACCTATAAAAAATAGCGGTATCACGAGGCCCTTTTCTG	5881
Db	5733	GAAACCATTTATCATGACATTAACCTATAAAAAATAGCGGTATCACGAGGCCCTTTTCTG	5792
QY	5882	C 5882	
Db	5793	C 5793	

RESULT 7
US-08-893-327-19
; Sequence 19, Application US/08893327
; Patent No. 6020192
; GENERAL INFORMATION:
; APPLICANT: Zolotukhin, Sergei

Db 3769 AAAGATACACAGGGGTTTCCCGCTGGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCCCTGC 3828
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Db 3829 CGCTTACCGGATACCTGTCCGCTCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCT 3888
Qy 4263 CAGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCTTCCGCTCAAGCTGGGTGTGTGACG 4322
Db 3889 CAGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCTTCCGCTCAAGCTGGGTGTGTGACG 3948
Qy 4323 AACCCCGCTTCAGCGCGACCGCTGGCGCTTATCCGCTACTATCGTTCGTAGTCCCAAC 4382
Db 3949 AACCCCGCTTCAGCGCGACCGCTGGCGCTTATCCGCTACTATCGTTCGTAGTCCCAAC 4008
Qy 4383 CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATAGCAGACGA 4442
Db 4009 CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATAGCAGACGA 4068
Qy 4443 GGTATGAGCGGTGTACAGAGTTCCTGAAGTGTGGCTTAACCTACGCGCTACACTAGAA 4502
Db 4069 GGTATGAGCGGTGTACAGAGTTCCTGAAGTGTGGCTTAACCTACGCGCTACACTAGAA 4128
Qy 4503 GGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGAGTTGGTA 4562
Db 4129 GGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGAGTTGGTA 4188
Qy 4563 GCTCTTGATCCGCAACAAACACACCGCTGCTGAGCGTGGTTTTTGTGTTGCAAGCAGC 4622
Db 4189 GCTCTTGATCCGCAACAAACACACCGCTGCTGAGCGTGGTTTTTGTGTTGCAAGCAGC 4248
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Db 4249 AGATTACGCGCAGAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACCGGCTGTG 4308
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Db 4309 ACCCTCAGTGGACGAAACCTCAGTTAGGGATTTTGTGTCATGAGTATCAAAAAGGA 4368
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Db 4429 AGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTAGGCGACCTATCTCAGCGATCT 4488
Qy 4863 GTCTATTTGGTTCATCCATAGTTGCTGACTCCCGTCTGTTAGATAACTACGATACGG 4922
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Db 4609 CAGATTATCAGCAATAAACCCAGCCAGCGGAAGGCGCAGACGAGTGGTCTGCA 4668
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Db 4669 CTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAGCTAGAGTAAGTTCG 4728
Qy 5103 CAGTTAATAGTTTGGCAACGTTTGGCCATCTGCTACAGCATCGTGGTGTACGCTCGT 5162
Db 4729 CAGTTAATAGTTTGGCAACGTTTGGCCATCTGCTACAGCATCGTGGTGTACGCTCGT 4788
Qy 5163 CGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAGCATCAAGCGCAGTTACATGATCCC 5222
Db 4789 CGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAGCATCAAGCGCAGTTACATGATCCC 4848
Qy 5223 CCATGTTGCAAAAAAGCGGTTAGCTCTTTCGGTCTCGATCGTGTGTCAGAGTAAGT 5282
Db 4849 CCATGTTGTCAAAAAGCGGTTAGCTCTTTCGGTCTCGATCGTGTGTCAGAGTAAGT 4908

RESULT 8

US-08-893-327-17
; Sequence 17, Application US/08893327
; Patent No. 6020192
; GENERAL INFORMATION:
; APPLICANT: Zolotukhin, Sergei
; APPLICANT: Hauswirth, William W.
; APPLICANT: Muzyczka, Nicholas
; TITLE OF INVENTION: Humanized Green Fluorescent Protein
; TITLE OF INVENTION: Genes and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,201
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UFLA:062\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 988..1728
; US-08-893-327-17

Query Match      37.8%; Score 2225.6; DB 3; Length 6280;
Best Local Similarity 65.2%; Pred. No. 0;
Matches 3518; Conservative 0; Mismatches 1809; Indels 67; Gaps 14;

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Db 176 GGTACCCTTACATAACTTACGGTAATAATGGCCCGCTGGCTGACCGCCCAACGACCCCG 235
QY 555 CCCATTGACGTCMAATAAGCATGATGTTCCCATAGTAAGCCCAATAGGACATTTCCATTG 614
Db 236 CCCATTGACGTCMAATAAGCATGATGTTCCCATAGTAAGCCCAATAGGACATTTCCATTG 295
QY 615 ACGTCAATGGGTGGAGTATTACGTTAAACTGCCACATTTGGGAGTACATCAAGTGTATCA 674
Db 296 ACGTCAATGGGTGGAGTATTACGTTAAACTGCCACATTTGGGAGTACATCAAGTGTATCA 355
QY 675 TATGCCAAGTCCGCCCCCTATTGACGTCMAATGACGGTAATAATGGCCCGCTGGCATTTATGC 734
Db 356 TATGCCAAGTACGCCCCCTATTGACGTCMAATGACGGTAATAATGGCCCGCTGGCATTTATGC 415
QY 735 CCAGTACATGACCTTACGGGACTTTCTACTTGGCAGTACATCTAGTATTAGTCATCGC 794
Db 416 CCAGTACATGACCTTACGGGACTTTCTACTTGGCAGTACATCTAGTATTAGTCATCGC 475
QY 795 TATTACCATGTTGATCGGTTTTGGCAGTACACCAATGGCGTGGATAGCGTTTGACCTC 854
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Db 596 TCNAACGGGACTTTCNAATATGCTGAATAAACCCCGCCCGTTGACCAAAATGGCGGCTAG 655
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QY 1095 CGCCCGGGAACGGTGCATTGGAAACGGGATTCGCCGTGCAAGAGTACGTAAGTACCGC 1154
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QY 1155 CTATAGACTCTATAGGACACACCCCTTTGGCTCTTATGTCATGCTATCTGTTTGGCTTG 1214
Db 816 AAGTTTAACTGGTAAGTTTATGCTTTTGTCTTTTATTTTTCAGTCCCGGATCCGGTGGTG 875
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1116 AGGTGATGCCACATACGGAAGCTCACCTCGAAATTCATCTGCACCACTGGAAGAGTCCC 1175
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1176 TGTGCCATGGCCAAACACTGGTCACTACCTGACCTATGGCG--TGCAGTGTCTTTCCAGA 1233
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1294 CAGGAGAGAACCATCTTTTTTCAAGATGACGGGAATCAAGACCCGCGCTGAAGTCAAG 1353
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2054 GCCCAGCGCTAGCAAAACCCACGTCACCGGGGGAAGTGC CGGCCACACTGTGTGGAAT 2113
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2114 TGTTAGCTCTCTCGCACGAGCGCCAGCAGAAAGCTGCTGAGTCAACACCAACCGAG 2173
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1894 TTCAATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGAGGTTTTTTTAGTCGACTCGAGCA 1953
2293 GCCGACCCCTTACCGATTTTGAACGAGGCTGGGGCCCTATCAGTTATGCAACGAGAGCG 2352
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2353 GCCCGACGAGCGCCCTACTGCTGCACTACCCCCCAAAACCTTGGCGGTATTGTGCCCG 2412
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2071 GGAA---TGTTTCCACCCAAATGCGAGCAACCCCGCCAGCGTCTGTCAATGGCAAT 2127
2473 CCAGCAGGTGGGGGGCCCACTACAGCTGGGGTGAATAATGATACGGAGCTCTCGTCC 2532
2128 CGAACGCGAGATGCACTGGGGGGCGGTCCAGGTCCACTTCGCATATTAAGGTGA 2187
2533 TTAACAAATACCGACCAACCGCTGGGCAATGGTTGGTTGGTTGATCTGGATGAATCAACTG 2592
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2652 CTGCACTGCCCCCACTGATTGCTTCCGCAAGCATCCGAGCCACATACTCTCGGTGGC 2711
2308 GCACACAGACATCGCTGCTGATGCCCGGTGTTCCGGCTGTACGGCGCAGGGGCGC 2367
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2605 CATAAG-CTTGATCCGGTCTACCTGCCCATTCGACCAACAAAGCGAAATCGCAT 2657
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3187 CTGAGTAGGTGCTATTTCTTCTTCTGGGGTGGGGTGGGCGAGCAGCAAGAGGGAGGAT 3246
3609 TAGAAGGCGCGCAAGATATCAAGGATCCACTACGCTTAGAGTCTCGTGATCAGCCTC 3668
3247 TGGGAAGACAATAGCAGGCACTGCTGGGAGAGATCTAGGAACCCCTAGTGATGAGTTGG 3306
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4015 GACGACCTTATCGCCACTGGGAGGAGCCACTGGTAAACAGGATTAACAGAGCGAGGTATG 4074
4449 TAGGCGGTCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCTACACTAGAGGACAG 4508
4075 TAGGCGGTCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCTACACTAGAGGACAG 4134
4509 TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAGAGTTGGTAGTCTTT 4568
4135 TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAGAGTTGGTAGTCTTT 4194

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DB GATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTCCAAAGCAGCAGATTA 4254
QY 4629 CGCGCAGAAAAAAGGATCTCAAGAGATCCCTTTGATCTTTTCTACGGGGTCTGAGCGTC 4688
DB CGCGCAGAAAAAAGGATCTCAAGAGATCCCTTTGATCTTTTCTACGGGGTCTGAGCGTC 4314
QY 4689 AGTGGAAAGAAACCTCAGCTTAAGGATTTTGGTCATGAGATTTATCAAAAAGGATCTTCA 4748
DB AGTGGAAAGAAACCTCAGCTTAAGGATTTTGGTCATGAGATTTATCAAAAAGGATCTTCA 4374
QY 4749 CCTAGATCTTTTAAATTAATAAGATTTTAAATCAATCAATCAATCAATCAATCAATCAAT 4808
DB CCTAGATCTTTTAAATTAATAAGATTTTAAATCAATCAATCAATCAATCAATCAATCAAT 4434
QY 4809 CTGTGCTCAGAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGCTAT 4868
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DB TTGCTTCATCCATAGTTGCTGACTCCCGTCTGCTAGATAACTAGTACGAGGGGCT 4554
QY 4929 TACCATCTGGCCCGAGTGTGCAATGATACCGGAGACCCAGCTCACCAGGCTCCAGATT 4988
DB TACCATCTGGCCCGAGTGTGCAATGATACCGGAGACCCAGCTCACCAGGCTCCAGATT 4614
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DB TATCAGCAATAAACACGAGCGGAGGCGGAGGCGGAGAGTGTCTGCAACTTTAT 4674
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QY 5109 ATAGTTTGGCAACGTTGTTGCCATTTGCTACAGGCATCTGTGTGTCACGCTCGTGTGTTG 5168
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DB GTATGCTTTCTTACGCTCCGTTTCCAAACGATCAAGGCGAGTTACATATCCCCATCT 4854
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RESULT 9
US-08-893-327-15
; Sequence 15, Application US/08893327
; Patent No. 6020192
; GENERAL INFORMATION:
; APPLICANT: Zolotukhin, Sergei
; APPLICANT: Hauswirth, William W.
; APPLICANT: Muzyczka, Nicholas
; TITLE OF INVENTION: Humanized Green Fluorescent Protein
; TITLE OF INVENTION: Genes and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,201
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UFLA:062\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6253 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 988..1701
; US-08-893-327-15

Query Match 37.8%; Score 2220.6; DB 3; Length 6253;
Best Local Similarity 65.9%; Pred. No. 0;
Matches 3566; Conservative 0; Mismatches 1719; Indels 124; Gaps 19;

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QY 236 CCATTGACGTCATTAATGATGATGTTCCATAGTAAGCCCAATAGGACCTTTCCATTG 295
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QY 1589 TGTCCACCCAGTCTGCCCTGTCTAAGATCCCAACGAAAGAGAGACCATGCTCTGTC 1648
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QY 1984 AAGCAATCATGATGCAATGAAGAGAGGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2043
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QY 2104 TGTCTGGAATTTGTAGCTCTCGCACAGGCGCCCAAGCAAGACGTCACAGCTCATCAACA 2163
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RESULT 10

US-09-132-808-1

; Sequence 1, Application US/09132808

; Patent No. 6197332

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; GENERAL INFORMATION:
; APPLICANT: Ronald Zuckermann et al.
; TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related
; TITLE OF INVENTION: Compositions and Methods Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/132,808
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1387.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4328 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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US-09-132-808-1

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Query Match 36.8%; Score 2166.4; DB 3; Length 4328;
Best Local Similarity 70.4%; Pred. No. 0;
Matches 3060; Conservative 0; Mismatches 1236; Indels 52; Gaps 10;
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Qy 333 GGAATTTATGGCTATGGCCATTTGCATAGCTTGTATCTATATCATATAATGTACATTTA 392
Db 4 GCGGAATTTCCAGTCTTAGGCCATTGCATAGCTTGTATCTATATCATATAATGTACATTTA 63
Qy 393 TATTGCTCATGTCCCATATGACCGCCATGTTCACATTTGATTATGACTAGTTATTATA 452
Db 64 TATTGCTCATGTCCCATATGACCGCCATGTTCACATTTGATTATGACTAGTTATTATA 123
Qy 453 GTAATCAATTTACGGGGTTCATTAGTTTCATAGCCCATATATGGAGTTCGCGCTTACATAACT 512
Db 124 GTAATCAATTTACGGGGTTCATTAGTTTCATAGCCCATATATGGAGTTCGCGCTTACATAACT 183
Qy 513 TAGCGTAATGGCCCGCTGGCTGACCGGCCAAGACCCCGCCCATTTGACGTCATTAAT 572
Db 184 TAGCGTAATGGCCCGCTGGCTGACCGGCCAAGACCCCGCCCATTTGACGTCATTAAT 243
Qy 573 GAGTATGTTCCCATAGTAACGCCAATAGGAGCTTTCCATTGACGTCATTAATGGGTGGAGTA 632
Db 244 GAGTATGTTCCCATAGTAACGCCAATAGGAGCTTTCCATTGACGTCATTAATGGGTGGAGTA 303
Qy 633 TTTACGGTAAACTGCCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCC 692
Db 304 TTTACGGTAAACTGCCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCC 363
Qy 693 TATTGACGTCATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTACATGACCTTACG 752
Db 364 TATTGACGTCATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTACATGACCTTACG 423
Qy 753 GGACTTTCTTACTTGGCAGTACATCTACGTTATTAGTCATCGCTATTACCATGGTGTGCG 812
Db 424 GGACTTTCTTACTTGGCAGTACATCTACGTTATTAGTCATCGCTATTACCATGGTGTGCG 483
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Qy	913	GT	TTTGGCAGTACACCAATGGCGCTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCT	872
Db	484	GT	TTTGGCAGTACACCAATGGCGCTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCT	543
Qy	873	CC	ACCCCAATTGACGTCGAATGGAGGTTTTGTTTGGCACCAAAATCAACGGGACNTTCCAAA	932
Db	544	CC	ACCCCAATTGACGTCGAATGGAGGTTTTGTTTGGCACCAAAATCAACGGGACNTTCCAAA	603
Qy	933	AT	GTCTGAATAAACCCCGCCCGTTTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGT	992
Db	604	AT	GTCTGAATAAACCCCGCCCGTTTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGT	663
Qy	993	CT	ATATAAGCAGAGCTCGTTTAPGTGAACCGGTACAGTCCGCTGGAGACGCCATCCACGCTG	1052
Db	664	CT	ATATAAGCAGAGCTCGTTTAPGTGAACCGGTACAGTCCGCTGGAGACGCCATCCACGCTG	723
Qy	1053	TTTT	TGACCTCCATAGAGACACCCGGGACCGATCCAGCTCCGGCGCCGGGAAACGGTGCAT	1112
Db	724	TTTT	TGACCTCCATAGAGACACCCGGGACCGATCCAGCTCCGGCGCCGGGAAACGGTGCAT	783
Qy	1113	TG	GAACCGGGATCCCGCTGCCAAGAGTGACGTAAGTACGCCCTATAGACTCTATAGGCA	1172
Db	784	TG	GAACCGGGATCCCGCTGCCAAGAGTGACGTAAGTACGCCCTATAGACTCTATAGGCA	843
Qy	1173	CAC	CCCTTTTGGCTCTATGCAATGCTATACTGTCTTTTGGCTTTGGGCGCTATACACCCCGC	1232
Db	844	CAC	CCCTTTTGGCTCTATGCAATGCTATACTGTCTTTTGGCTTTGGGCGCTATACACCCCGC	903
Qy	1233	TC	CTTATGCTATAGGTGATGTATAGCTTAGCCCTATAGGTGTGGGTTATTGACCATTAATT	1292
Db	904	TC	CTTATGCTATAGGTGATGTATAGCTTAGCCCTATAGGTGTGGGTTATTGACCATTAATT	963
Qy	1293	GAC	CACCTCCCTATTGTTGAGCATCTTTCCATTACTAAATCCATAACATGCTCTTTGGC	1352
Db	964	GAC	CACCTCCCTATTGTTGAGCATCTTTCCATTACTAAATCCATAACATGCTCTTTGGC	1023
Qy	1353	ACAA	CTATCTCTATTGGCTATATGCCAATACTCTGTCTTTGAGAGACTGACGGAAGTCT	1412
Db	1024	ACAA	CTATCTCTATTGGCTATATGCCAATACTCTGTCTTTGAGAGACTGACGGAAGTCT	1083
Qy	1413	GTAT	TTTTTACAGGATGGGTCCATTTATTTATTTACAAATTCACATATACAAACACGCCGT	1472
Db	1084	GTAT	TTTTTACAGGATGGGTCCATTTATTTATTTACAAATTCACATATACAAACACGCCGT	1143
Qy	1473	CCCC	GTGCGCGAGTTTTTATTAACATAGCGTGGGATCTCCGACATCTCGGTACGCTG	1532
Db	1144	CCCC	GTGCGCGAGTTTTTATTAACATAGCGTGGGATCTCCGACATCTCGGTACGCTG	1203
Qy	1533	TTCC	GGACATGGGCTCTTTCCGGTAGCGGGAGCTTTCCACATCCGAGCCCTGGTCCCA	1592
Db	1204	TTCC	GGACATGGGCTCTTTCCGGTAGCGGGAGCTTTCCACATCCGAGCCCTGGTCCCA	1263
Qy	1593	TCCG	TCCAGCGGCTCATGCTCGCTCGGAGCTCTCTTGTCTTAACAGTGAGGCGCAGACT	1652
Db	1264	TCCG	TCCAGCGGCTCATGCTCGCTCGGAGCTCTCTTGTCTTAACAGTGAGGCGCAGACT	1323
Qy	1653	TAGC	CACAGCAATGCCACCAACAGTGTCGCGCACAGGCCCTGGCGGTAGGGTA	1712
Db	1324	TAGC	CACAGCAATGCCACCAACAGTGTCGCGCACAGGCCCTGGCGGTAGGGTA	1383
Qy	1713	TGTG	TCTGAAATGAGCTCGAGATTTGGGCTCGCACTTGAACGAGATGGAAGACTTAAG	1772
Db	1384	TGTG	TCTGAAATGAGCTCGAGATTTGGGCTCGCACTTGAACGAGATGGAAGACTTAAG	1443
Qy	1773	GCAC	GGCAGAAAGATGCAAGGACGCTGAGTTGTTGTTATTTGATTAAGAGTCAAGGTA	1832
Db	1444	GCAC	GGCAGAAAGATGCAAGGACGCTGAGTTGTTGTTATTTGATTAAGAGTCAAGGTA	1503
Qy	1833	ACTC	CCGTTGCGGTCGTTTAAACGTTGGAGGCGAGTGTAGTCTTGACGAGTACTCGTTGCT	1892
Db	1504	ACTC	CCGTTGCGGTCGTTTAAACGTTGGAGGCGAGTGTAGTCTTGACGAGTACTCGTTGCT	1563
Qy	1893	GCCG	CGCGGCCACACATATAGCTGACAGACTAACAGACTGTGTTCTTTTCCATGGGT	1952

1564	Db	 GCCGCGCGCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCTCTTCATGGGT	1623
1953	Qy	CTTTTCTGCAGTCACCGTCTGTCACGAAATTCACAGCAATCATGGATGCAATGAAGAGAGGG	2012
1624	Db	CTTTTCTGCAGTCACCGTCTGCACCTAA-----GAATTCAGACTCGA	1666
2013	Qy	CTCTGCTGTGTGCTGTGTGTGGAGCAGTCTTCTGTTTGCGCCAGCGCTACGCAAAACC	2072
1667	Db	GCAAGTCTAGAAAGCCATGGATATCGGATCCACTACGCGTTAGAGCTCGCTGATCAGCCT	1726
2073	Qy	CAGCTCACCGGGGGAGTGC CGGCGCACATGTGTCTGGAATTTGTTAGCTCTCTCGCACCA	2132
1727	Db	CGACTGTGCCCTTCTAGTTGCGACGCCATCTGTTGTTTGCCTCCCGCGTGCCTTCTCTTGA	1786
2133	Qy	GGCGCAGCAGAAACGTCGACGCTGATCAACACCAACGGCAGTTGGCAGCTCTCAATAGCAACG	2192
1787	Db	CCCTGGAAGGTGCCACTCCCACTGTCTTCTCTAAATAAGGAAATTCATCGCGATT	1846
2193	Qy	GCCCTGAATGCAATGATAGCTCAACACCGGCTGTGTGCGAGGGCTTTTCTATCACCAC	2252
1847	Db	GTCTG-----AGTAGGTCTATTCTATCTGGGGGTGGGTGGGGCAGGACAGC	1896
2253	Qy	AAGTTCAACTCTTCAGGCTGCTCTGAGAGCTTAGCAGCTGCCGACCCCTTACCGATTTT	2312
1897	Db	AAGGGGAGGATTTGGGAAGACAATAGCAGGGGGTGGCGGAAGAACTCCAGCATGAGATC	1956
2313	Qy	GACACGGCTGGGGCCCTATCAGTTATGCCAAACGGAAGCGGCCCGCAGCAGCGCCCTAC	2372
1957	Db	CCGCGCTGAGGATCATCAGCGCGCGTCCCGGAAACGATTCGGAAGCCCAACCTTTC	2016
2373	Qy	TGCTGGCATTACCCCCCAAAACCTTCGCGTATTGTGCCCGCGAAGAGTGTGTGTCGCG	2432
2017	Db	ATAGAAGCGCGGTGGAA---TCGAAATCTCGTATGCGCAGGTTGGGCGTCGCTTGGT	2072
2433	Qy	GTATATGCTTACTCCACGCCCGTGTGGTGGGAACGACAGTGTGGGGCGGCGCC	2492
2073	Db	CGGTCATTTCCGAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGGCGATAGAAGGC	2132
2493	Qy	ACCTACAGCTGGGGTGAATATGATACGGAGCTTCTCGTCTTAAACAATACCGGCCACCG	2552
2133	Db	GATGCGCTGGAATCGGAGCGGCGATACCGTAAAGCAGCAGGAAGGGTGCACCCATTC	2192
2553	Qy	CTGGGCAATTTGGTTTCGTTGTAAGTCTGAACTCAACTGGATTCACAAAGTGTGCGGA	2612
2193	Db	GCCGCCAAGCTCTTCAGCAATATCAGGGTAGCAACGCTATGCTCTGTATAGCGTCCG	2252
2613	Qy	GCSCCTCTTGTGTCTATCGAGGGGGGGGCAACACACCCCTGCAGTGCCTCCACTGATTCG	2672
2253	Db	CACACCAGCGCGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGAT--A	2310
2673	Qy	TTCCGCAAGCATCGGACGCCATATCTCTCGGTGGGCTCCGCTCCCTGGATCAGACCC	2732
2311	Db	TTCCGCAAGCAGGCATCGCCATCGGTTCAGCAGAGATCTCTCGCGCTCGGGCATTCGCGCC	2370
2733	Qy	AGTGTCTGTGTGACTACCCGTATAGCTTTGGCAATTATCTTGTACCACTCAACTACACC	2792
2371	Db	TTGAGCTTGGGAACAGTTTCGCTGGCGCGAGCCCTGATGCTCTTCGTCCAGATCATCC	2430
2793	Qy	ATATTTAAATACGATGTACGTGGAGGGGTGGAAACACAGGCTGGAAAGTGCCTGCAAC	2852
2431	Db	TGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGGCATGTTTCGCTGG	2490
2853	Qy	TGGACGGGGCGAAGTTCGATCTGGAGATAGGACAGGTCGAGATCGATATGGAG	2912
2491	Db	TGTCGGAATGGGAGGTAGCCGG-----ATCAAGGCTATGACAGCCCGCATTTGCATCA	2544
2913	Qy	AACATACATCAGGATTCCTAGGACCCCTGCTCGTGTAAAGCGGGGTTTTTCTTTGTTG	2972
2545	Db	GCAATGATGATCTTCTTCGGCAGGACGAAGGTGAGATGACAGAGAGATCTCTGCCCGGC	2604
2973	Qy	ACAAGAATCTCTCAATAACCGCAGAGCTAGACTCGTGTGGAGCTTCTCTCAATTTTCTA	3032


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; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4328 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-910-647-2

Query Match      36.8%; Score 2166.4; DB 3; Length 4328;
Best Local Similarity 70.4%; Pred. No. 0;
Matches 3060; Conservative 0; Mismatches 1236; Indels 52; Gaps 10;

QY 333 GGAAATATTGGCTATTGGCCATGTGATACGTTGTATCTATATCAATAATGTACATTTA 392
DB 4 GCGGAATTTGCACTCTAGGCCATTGTCATACGTTGTATCTATATCAATAATGTACATTTA 63

QY 393 TATTGGCTCATGCCAATATGACCGCCATGTTGACATTTGACTAGTTATTAAATA 452
DB 64 TATTGGCTCATGTTCCAAATATGACCGCCATGTTGACATTTGACTAGTTATTAAATA 123

QY 453 GTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCGGCGTTACATAACT 512
DB 124 GTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCGGCGTTACATAACT 183

QY 513 TAGCGTAAATGGCCGCTGGCTGACCGCCCAACGACCCCGCCCAATTGACGTCATAAAT 572
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DB 304 TTTACGGTAAACTGGCCACTTTGGCAGTACATCAAGTGTATCATATGCAAGTCCGCCCCC 363

QY 693 TATTGACGTCOAATGACGTTAAATGGCCGCTGGCATTTATGCCCAGTACATGACCTTTAGC 752
DB 364 TATTGACGTCOAATGACGTTAAATGGCCGCTGGCATTTATGCCCAGTACATGACCTTTAGC 423

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QY 813 GTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGTACTCAGCGGGAATTTCCAAAGTCT 872
DB 484 GTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGTACTCAGCGGGAATTTCCAAAGTCT 543

QY 873 CCACCCCATTTGACGTCOAATGGGAGTTTGTGTCGACCAAAATCAACGGGACTTTCCAAA 932
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DB 844 CACCCCTTTGGCTCTTATGATGCTACTACTGTTTGGCTTTGGGCGCTATACACCCCGC 903
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1024 ACAACTATCTCTATTGGCTATATGCCAATACTCTGTCTCTTCAGAGACTGACACGGACTCT 1083
1413 GTATTTTACAGATGGGGTCCATTATTATTATTAACAAATTCACATATACAAACGCCGT 1472
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1204 TTCCGACATGCGGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGTGCCA 1263
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1264 TCCGTCACAGCGGCTCATGCTCGGAGCTCTTGTCTCTTAAACAGTGGAGGCCAGACT 1323
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1727 CGACTGTGCTTCTAGTTGCGCAGCCATCTGTGTGTTGTCCTCCCGCTCCCTTCTTGA 1786
2133 GGGCCCAACAGCAGACGTCAGCTGATCAACACCGGCGTGTGGCAGGGCTTTTATCACCC 2192
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1897 AAGGGGAGGATTGGGAAGACAAATAGCAGGGGGGTGGGCGAAGAACTCCAGCATGAGATC 1956
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QY 2313 GACCAGGCTGGGGCCCTATCAGTTATGCCAAGCGGCGCCCGACACGCGCCCTAC 2372
DB 1957 CCCGCGTGGAGATCATCAGCGGGGTCCCGGAAACGATTCCGAAAGCCCAACCTTTC 2016
QY 2373 TGTGGCACTACCCCCCAAAACCTTGGGGTATTGTGCCCCCGGAAGAGTGTGTGGTCG 2432
DB 2017 ATAGAAGCGCGGTGGAA-----TCGAAATCTCGTGTATGGCAGGTTGGGGGTGCGTTGGT 2072
QY 2433 GTATATTGCTTCACTCCAGCGCGGTGGTGGGAAGACCGACAGGTGCGGCGGCC 2492
DB 2073 CGGTCAATTCGAACCCAGAGTCCGCTCAAGAAGACTCGTCAAGAAGCGGATAGAAGGC 2132
QY 2493 ACCTACAGCTGGGGTGAATATGATACGAGCTCTTGGTCTTAACTAACATACAGGCCACCG 2552
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DB 2431 TGATCGACAAGACGGGCTTCATCCGAGTAGCTCGCTCGATGCGATTTTCGCTGG 2490
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DB 2665 CAAGGAACGCGCTGCGGCGACGCCAGATAGCGCGCTGCTCGTCTGCACTTCA--- 2721
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DB 2840 GCCTCTCAACCAAGCGCGGAGAACCTGGTGATCATCATCTTGTTCATCATGCGAA 2899
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DB 2900 ACGATCTCATCTGTCTCTTG---ATCAGATCTTGATCCCTGCGGCATCAGATCTCTG 2956
QY 3333 ACGATGGAATTTGCACTGTATCCCATCTGCTGCTGCGGTTTTGCGCAAAATACCTA 3392
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QY 3393 TGGAGTGGGCGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTCAAGTG 3452

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QY 3453 TTGCTAGGCGTTTCCCGCACTGTTGGCTTTAGCTATATGATGATGTTGGGTATGGGG 3512
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DB 3137 CCAGTAGCTGACATTCATCCGGGTGAGCACCGCTTCTGCGGACTGSCCTTTCTACGTG 3196
QY 3571 TCTGGGTATACATTTAAGAAATTCAGACTCGAGCAAGTCTAGAAGGCGCCCAAGATATC 3630
DB 3197 TCGCTTCTTTAGCAGCCCTTGGCGCTGAGTGTCTTGGCGCAGCGTGAAGCTGTCAATT 3256
QY 3631 AAGGATCCACTAGCGGTAGAGCTCGCTGATCAGCCTCGACTGTGCTTCT--TAGTTGCC 3688
DB 3257 CCGCGTTAAATTTTGTAAATCAGCTCAATTTTAAACCAATAGGCGCAAAATCGGCAAA 3316
QY 3689 AGCATCTGTGTTTGGCCCTCCCGCTGCTTCTTTCACCCCTGGAAGGTGCCACTCCCA 3748
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QY 3749 CTGCTCTTCTTAATTAAGAAATTCGATCGCATTTGTCTGAGTGTGATGTCATTCTA 3808
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DB 3437 GCGATGCGCGATCAGCTTATGCGGTGTGAATATCCGACAGATGCGTAAGGAGAAATAC 3496
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DB 3497 CGCATCAGGCGCTTCTCGCTTCTCGCTCACTGACTCGCTGCGCTCGGCTGTTTCGGCTG 3556
QY 3929 CGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACCGACAGATGCGTAAGGAGAAATAC 3988
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QY 4049 GCGTCTGCGGCTTTTTCATAGGCTCCGCGCCCTGACGAGCATCACAAAATTCGACGC 4108
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QY 4109 TCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCGCTGGA 4168
DB 3737 TCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCGCTGGA 3796
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DB 3797 AGCTCTCTGCTGCTCTCTCTGTCGACGAAACCCCGCTTACCGGATACCTGTCGCGCTTT 3856
QY 4229 CTCCTTTCGGGAAGCGTGGCGCTTCTCAATGTCTACGCTGTAGGTATCTCAGTTCCGCTG 4288
DB 3857 CTCCTTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGCTG 3916
QY 4289 TAGGTCGTTGCTTCCAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGCGACCGCTGC 4348
DB 3917 TAGGTCGTTGCTTCCAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGCGACCGCTGC 3976
QY 4349 GCCTTATCCGTTAACTATGCTTGTAGTCCAAACCCGTTAAGACACGACTTATCGCCACTG 4408
DB 3977 GCCTTATCCGTTAACTATGCTTGTAGTCCAAACCCGTTAAGACACGACTTATCGCCACTG 4036
QY 4409 GCAGAGCCACTGCTAAACAGGATTAGCAGAGCAGGTATGTAGCGGTGTCTACAGAGTTC 4468
DB 4037 GCAGAGCCACTGCTAAACAGGATTAGCAGAGCAGGTATGTAGCGGTGTCTACAGAGTTC 4096
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Db 4097 TTGAAGTGGTGGCTAACTAGCGCTACACTAGAAGGACAGATATTTGGTATCTGGCTCTG 4156
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Db 4157 CTGAAGCCAGTTACTCTCGGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAAACCAACC 4216
Qy 4589 GCTGGTAGCGGTGGTTTTGTTGTCGACGACAGATTACGGCGCAGAAAAAAGGATCT 4648
Db 4217 GCTGGTAGCGCGG-TTTTGTGTTGTCGACGACAGATTACGGCGCAGAAAAAAGGATCT 4275
Qy 4649 CAAGAAGATCCTTTGATCTTTTCTACGG 4676
Db 4276 CAGAAGATCCTTTGATCTTTTCTACTG 4303

RESULT 12
US-09-620-925-2
; Sequence 2, Application US/09620925
; Patent No. 6468986
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; Polynucleotide Delivery
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/620,925
; FILING DATE: 21-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,647
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4328 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-620-925-2

Query Match 36.8%; Score 2166.4; DB 3; Length 4328;
Best Local Similarity 70.4%; Pred. No. 0;
Matches 3060; Conservative 0; Mismatches 1236; Indels 52; Gaps 10;

Qy 333 GGGAAATTATGGGTATTGGCCATTGCATAGCTTGTATCTATATCATATAATGTACATTTA 392
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Qy 393 TATTGGCTATGTCCAAATATGACGGCATTTGACATTTGATTAATGACTAGTTATTAATA 452
Db 64 TATTGGCTATGTCCAAATATGACGGCATTTGACATTTGATTAATGACTAGTTATTAATA 123
Qy 453 GTAATCAATACGGGGTCATTAGTTTCATAGCCCCCATATATCGAGTTCGGGTTACATAACT 512

Db 124 GTATCAATATTCGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGGCTTACATAACT 183
Qy 513 TACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCAATTGAACGTCATAAAT 572
Db 184 TACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCAATTGAACGTCATAAAT 243
Qy 573 GACGTATGTTCCCATAGTAACGCCAATAGGGAATTTCCATTGACGTCAATGGTGGAGTA 632
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Qy 633 TTTTACGGTAAACTGGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCC 692
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Qy 693 TATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTACG 752
Db 364 TATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTACG 423
Qy 753 GGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCG 812
Db 424 GGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCG 483
Qy 813 GTTTTGGCAGTACCAATGGCGCTGGATAGCGGTTTGACTCAGCGGGATTTCCAAAGTCT 872
Db 484 GTTTTGGCAGTACCAATGGCGCTGGATAGCGGTTTGACTCAGCGGGATTTCCAAAGTCT 543
Qy 873 CCACCCCATTTGACGTCAATGGGAGTTTGTTTGGCA CCAAAATCAACGGGACTTTCCAAA 932
Db 544 CCACCCCATTTGACGTCAATGGGAGTTTGTTTGGCACCAAAATCAACGGGACTTTCCAAA 603
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Db 724 TTTTGACCTCCATAGAAGACACCGGACCGATCCAGCTCCGCGCCGGAAACGGTGCAT 783
Qy 1113 TGGAAACGGGATTTCCCGTGCACCAAGTGA CTTAGTACCGCTATAGACTCTATAGGCA 1172
Db 784 TGGAAACGGGATTTCCCGTGCACCAAGTGA CTTAGTACCGCTATAGACTCTATAGGCA 843
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Db 1024 ACNACTATCTCTATTGGCTATATGCCAATACCTCTGTCCTTCAGAGACTCAGACGGACTCT 1083
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Db 1144 CCCCCGTGCGGAGTTTTTATTAACATAGCTGGGATCTCCGACATCTCCGGTACGCTG 1203
Qy 1533 TTCCGGACATGGGCTCTCTCTCCGGTAGCGCGGAGCTTCCACATCCGAGCCCTGGTCCCA 1592

Db 1204 TTCGGGACATGGGCTCTTCTCCGGTAGCGGGAGCTTCCACATCGAGCCCTGGTCCA 1263
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Db TCCGTCAGCGGCTCATGGTCGTCGCGAGCTCCTTGCTCTTAACAGTGGAGCCAGACT 1323
Qy TAGGCACAGCAATGCCACCAACCAACAGTGTGCCCAACAAGCCGCTGGCGGTAGGGTA 1712
Db TAGGCACAGCAATGCCACCAACCAACAGTGTGCCCAACAAGCCGCTGGCGGTAGGGTA 1383
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Qy CTCGTGTGTGTGTGTGTGTGGAGCAGTCTTGTTTCGCCCGCAGCTAGCGAAACC 2072
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Qy CTGGGCAATTTGGTTCGTTGTACTCGATGAACTCAACTGGATTCAACAAAGTGTGCGGA 2612
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Qy AGCATCTGTTGTTGCGGCTTCCCGCTGCTTTCAGCCCTGGAAGGTTGCCACTCCCA 3748
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QY 4469 TTGAAGTGGTGGCTAACTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTG 4528
Db 4097 TTGAAGTGGTGGCTAACTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTG 4156
QY 4529 CTGAAGCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACC 4588
Db 4157 CTGAAGCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACC 4216
QY 4589 GCTGGTAGCGGTGGTTTTTTTGTTCAGCAGCAGATTAACGCGCAGAAAAAAGGATCT 4648
Db 4217 GCTGGTAGCGGG- TTTTGTGTTGCAAGCAGCAGATTAACGCGCAGAAAAAAGGATCT 4275
QY 4649 CAAGAGATCCTTTGATCTTTTCTACGG 4676
Db 4276 CAAGAGATCCTTTGATCTTTTCTACTG 4303
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RESULT 13
US-09-620-260-1
; Sequence 1, Application US/09620260
; Patent No. 6569450
; GENERAL INFORMATION:
; APPLICANT: Ronald Zuckermann et al.
; TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related
; Compositions and Methods Thereof

```
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patenclin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/620,260  
FILING DATE: 09-Oct-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Fujita, Sharon M.  
REGISTRATION NUMBER: 38,459  
REFERENCE/DOCKET NUMBER: 1387.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 923-2706  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-620-260-1  
  
Query Match 36.8%; Score 2166.4; DB 4; Length 4328;  
Best Local Similarity 70.4%; Pred. No. 0;  
Matches 3060; Conservative 0; Mismatches 1236; Indels 52; Gaps 10;  
  
QY 333 GGGAAATTATGGCTATTGGCCATTGCATACGTTGTATCTATATCATTAATATGACATTAA 392  
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QY 693 TATTGACGTCATAGCAGGTAATGCGCCCTGCGCATTTATGCCAGTACATGACCTTACG 752  
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Db 424 GGACTTTCTTACTTGGCAGTACATCTACGTTATAGTCATCGCTATTACCATTGTTATGCG 483  
QY 813 GTTTTGGCAGTACACCAATGGCGGTGGATAGCGGTTTGACTCACGGGGATTTCCAAAGTCT 872  
Db 484 GTTTTGGCAGTACACCAATGGCGGTGGATAGCGGTTTGACTCACGGGGATTTCCAAAGTCT 543
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Qy	873	CCACCCATTTGACGCTCAATGGGAGTTTGT	TTTGGGCA	CCAAAA	TCAACGGGAC	TTTCCAAA	932
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Qy	933	ATGTGCTAATAAACCCGCCCGT	TGACGCAAA	TGGGCGGTAGGCGTCTACG	GTGGGAGGT	992	
Db	604	ATGTGCTAATAAACCCGCCCGT	TGACGCAAA	TGGGCGGTAGGCGTCTACG	GTGGGAGGT	663	
Qy	993	CTATATAAGCAGAGCTCGT	TTAGTGAACCGT	CAGATCGCTGGAGACGCCAT	CCACGCTG	1052	
Db	664	CTATATAAGCAGAGCTCGT	TTAGTGAACCGT	CAGATCGCTGGAGACGCCAT	CCACGCTG	723	
Qy	1053	TTTGTGACCTCCATAGAGACACCGG	GCAGATCCAGCGCTCGCGGCGGGAA	CGGTGCTAT	1112		
Db	724	TTTGTGACCTCCATAGAGACACCGG	GCAGATCCAGCGCTCGCGGCGGGAA	CGGTGCTAT	783		
Qy	1113	TGGAACCGGGATTCCC	CGGTCCAAAGAGTGAC	TAAAGTACCGCCCTATATAGACTCTAT	TAGGCA	1172	
Db	784	TGGAACCGGGATTCCC	CGGTCCAAAGAGTGAC	TAAAGTACCGCCCTATATAGACTCTAT	TAGGCA	843	
Qy	1173	CACCCCTTTGGCTCTTATG	CATGACTACTGT	TTTTTGGCTTTGGGCGCTATAC	CACCCCGC	1232	
Db	844	CACCCCTTTGGCTCTTATG	CATGACTACTGT	TTTTTGGCTTTGGGCGCTATAC	CACCCCGC	903	
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Db	904	TCCTTATGCTATAGGTGATGGTATAG	CTTAGCCTATAGGTGTGGGTATTG	ACATATT	963		
Qy	1293	GACCACTCCCTATT	TGCTGACGATCTTTCCAT	TACTTAATCCATAACATGGCTCTTTGCC	1352		
Db	964	GACCACTCCCTATT	TGCTGACGATCTTTCCAT	TACTTAATCCATAACATGGCTCTTTGCC	1023		
Qy	1353	ACAACTATCTCTAT	TGGCTATATGCCAA	TACTCTGTCTTTACAGAGCTGAC	ACGGA	1412	
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Db	1264	TCGCTCAGCGGCTCAT	GTGTCGCTCGGACGCTCCTT	CCTAACAGTGGAGCCAGACT	1323		
Qy	1653	TAGSCACAGCACAA	TGCCACCA	CCACCAAGTGTGCGCACAAAGCCCGTGGCGGTAGGGGTA	1712		
Db	1324	TAGSCACAGCACAA	TGCCACCA	CCACCAAGTGTGCGCACAAAGCCCGTGGCGGTAGGGGTA	1383		
Qy	1713	TGTGTCTGA	AAATAGAGCTCGGAGATTGGGCTCGGAC	CTCTGGA	CGGAGATGGAAGCTTAAG	1772	
Db	1384	TGTGTCTGA	AAATAGAGCTCGGAGATTGGGCTCGGAC	CTCTGGA	CGGAGATGGAAGCTTAAG	1443	
Qy	1773	GCAGCGCAGAA	GAAGATG	CAGG	CAGCTGAGTTTGTGTA	TTCTGATAAGAGT	1832
Db	1444	GCAGCGCAGAA	GAAGATG	CAGG	CAGCTGAGTTTGTGTA	TTCTGATAAGAGT	1503
Qy	1833	ACTCCGCTTGGGTGCTGTT	TAACGGTGGAGGGCAGTG	TAGTCTG	CAGCAGTACTCGTTGCT	1892	
Db	1504	ACTCCGCTTGGGTGCTGTT	TAACGGTGGAGGGCAGTG	TAGTCTG	CAGCAGTACTCGTTGCT	1563	
Qy	1893	CGCGCGCGCGCCAC	CAGACATATATAGCTG	ACAGACTAA	CAGACTGTCTTTCCATGGGT	1952	
Db	1564	CGCGCGCGCGCCAC	CAGACATATATAGCTG	ACAGACTAA	CAGACTGTCTTTCCATGGGT	1623	

Qy	1953	CTTTTCTGCACTCACCGTCTGTCAGCAAGATTCACAGCAATCATGATGCATATGAAGAGAGGG	2012
Db	1624	CTTTTCTGCACTCACCGTCTGTCAGCAATTCACAGCAATCATGATGCATATGAAGAGAGGG	1666
Qy	2013	CTCTGCTGTCTGCTGCTGTGTGGAGCAGTCTTGGTTTGCAGCAGTCTTGGTTTGCAGCAGCGCTAGCGAAACC	2072
Db	1667	GCAAGTCTAGAAAGCCATGATATCGGATCCACTACGCTTACGCTTACGCTTGCATCAGCCT	1726
Qy	2073	CAGCTCACCGGGGGAAGTGCAGGCGCACACTGTGTCTGGAATTTGTATTACCTCTCTCGCACCA	2132
Db	1727	CGACTGTGCTTCTTAGTTGCGAGCCATCTGTGTGTGGCCCTCCCGCGTGCCTTCCCTTGA	1786
Qy	2133	GGCCCAAGCAGAACGTCAGCTGATCAACACCAACGAGGAGTTGGCACTCAATAGCAGC	2192
Db	1787	CCCTGGAAGTGCACCTCCCACTGTCTCTTAATAAATGAGGAAATGSCATCGCATTT	1846
Qy	2193	GCCCTGAAGTCAATGATAGCCTCAACACCGGCTGGTTGACAGGGCTTTTCTATCACCAC	2252
Db	1847	GTCTG-----AGTAGGTGTCTTCTTCTTGGGGGTGGGGTGGGGCAGGACGC	1896
Qy	2253	AAGTTCAACTCTTTCAGGCTCTCTCGAGAGCTAGCCAGTCCGACGCCCTTACCGCATTTT	2312
Db	1897	AAGGGGAGGATTTGGGAAGACAATAGCAGGGGGTGGCGCAAGACTCCACAGCATGAGATC	1956
Qy	2313	GACAGGGCTGGGGCCCTATCAGTTATGCCAAGCGAGCGGCCCGACACAGCGCCCTAC	2372
Db	1957	CCCGCTGTGAGGATCATCCAGCGCGGCTCCCGGAAACGATTCGGAAGCCCAACCTTTC	2016
Qy	2373	TGCTGGCACTACCCCCAAAACCTTCGGGTATTTGTCGCCGCGAAGAGTGTGTGTCGG	2432
Db	2017	ATGAAGCGCGCGGTGGAA----TCGAAATCTCTGTGATGGCAGTTTGGGGTGCCTTGGT	2072
Qy	2433	GTATATTGCTTCACTCCAGCCCGCTGGTGGTGGGAACGACCGACAGGTTCGGCGCGCCCC	2492
Db	2073	CGGTCAATTCGAACCCAGAGTCCCGCTCAGAGAGACTCGTCAAGAGGCGATAGAAGC	2132
Qy	2493	ACCTACAGCTGGGGTGAAAATGATACGGACGTCTTCGTCTCTTAACAAATACAGGCGCACCG	2552
Db	2133	GATCGCTGCGAATTCGGAGCGCGATACCGTAAAGCACAGGAAGCGGTTCAGCCCATTC	2192
Qy	2553	CTGGGCAATTTGGTTTCGTTCTACTCTGGATGAACTCAACTGGATTCACCAAGTGTGCGGA	2612
Db	2193	GCGGCCAAGCTCTTCAGCAATATACCGGTAGCCAAAGCTATGTCTCTGATAGCGGTCCGC	2252
Qy	2613	GCGCCTCTTGTCTATCGAGAGGGGGGCAACAAACCCCTGCACCTGCCCCACTGATTGC	2672
Db	2253	CACACCAGCGCGCCACAGTCGATGATATCCAGAAAGCGGCCATTTTCCACCATGAT--A	2310
Qy	2673	TTCCGCAAGCATCCGGAAGCAATCTCTCGGTGGGGTCCGGTCCCTGGATGATCAACCC	2732
Db	2311	TTCCGCAAGCAGGATCCGCATGGGTACGACAGATCTCTCGCGCTCGGGCATGCGCGCC	2370
Qy	2733	AGTGCCTGTGCACTACCGGTATAGCTTTGGCATTTATCTTTGTACCATCAACTACCC	2792
Db	2371	TTGAGCCTCGGCAACAGTTCGGCTGGCGGAGCCCTCGATGCTCTTCGTCCAGATCATCC	2430
Qy	2793	ATATTTAAATCAGATGTACGTGGAGGGGTGCAACACAGGCTGGAAGCTGCCTGCAAC	2852
Db	2431	TGATCGACAAGAAGGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTGGCTTG	2490
Qy	2853	TGGAAGCGGGGCAAGCTTGCATCTCGAAGATAGGGAAGAGTCCGAGATGATATGGAG	2912
Db	2491	TGGTTCGAATGGGAGGTAGCCGG-----ATCAAGCGTATGACGCGCGCATTCATCA	2544
Qy	2913	AACATCACATCAGGATTCCTAGAACCCCTGCTCGTGTACAGCGGGGGTTTTTCTTGTG	2972
Db	2545	GCCATGATGATATCTTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGGC	2604
Qy	2973	ACAAGAACTCTCAATATCCGACAGGTCTAGACTCGTGTGGTGAATCTCTCTCAATTTCTA	3032
Db	2605	ACTTCGCCCAATAGACGCAAGTCCCTTCCGCTTCTAGTGACAAACGTGACGACAGCTGGC	2664
Qy	3033	GGGGGATCTCCCGTGTCTTTGGCCAAAATTCGCAGTCCCCAACTCCCATCACTCACCA	3092

Db 2665 CAAGGAACGCCCGCTGTCGCGCAGCAGATAGCCGCGCTGCTCGCTCGCAGTTCA--- 2721
QY 3093 ACCTCCTGTCCTCAATTTGTCTCGTGTATTCGCTGGATGTGTCTGGGGCTTTTATCAT 3152
Db 2722 --TTCAGGGCACCGGACAGTCGGTCTTGACAAAAGAACCGGGCGCCCTGCGCTGACA 2779
QY 3153 TTCTCTTCACTCTGCTGTATGCTCCTCATCTTCTTATTTGGTCTTCTGGATTTCAAGGT 3212
Db 2780 GCCGGAACACGGCGGCATCAGACAGCCGATTTGCTGTTGTGCCCATCATAGCCGAATA 2839
QY 3213 ATGTTGCCCGTTTGTCTCTTAATTCAGGATCAACAACACAGTACGGGACCATCAAA 3272
Db 2840 GCCTCTCCACCCAGCGCGGAGAACCTGCGTGCATTCATCTTTTCAATCATCGGAA 2899
QY 3273 ACCTGACGCACTCTCTGCTCAAGCAACTCTATTTTCCCTCAATGTTGCTGTACAAAACCT 3332
Db 2900 ACGATCCTCATCTGCTCTTG--ATCAGATCTTGATCCCTGCGCCATCAGATCCTTG 2956
QY 3333 ACGGATGGAAATTGCACCTGTATTCGATCCCATCGTCTGCGGCTTTCGCAAAATACCTA 3392
Db 2957 GCGCAAGAAAGCATCCAGTTTACTTTGCAAGGCTTCCCAACCTTTACCAGAGGGCGCC 3016
QY 3393 TGGGAGTGGSCCTCAGTCGCTTTCTCTGCTCAGTTTACTAGTGCATTTGTTCAAGTG 3452
Db 3017 CAGCTGGCAATTCGGTTCGCTGCTGTGCTCAATAAAACCGCCCATGCTAGCTATCGCCATG 3076
QY 3453 TTCTGAGGGCTTTCCGCCACTGTTTGGCTTTTCAGCTATATGATGATGTGTTATTTGGGG 3512
Db 3077 TAAGCCCACTGCAAGCTACCTGCTTTCTCTTTCGCTGCTGCTTTCCCTTGCCAGATAG 3136
QY 3513 CAAAGT--CTGTACAGATCGTGAGTCCCTTTATACCGTGTGTACCAATTTCTTTTGTGTC 3570
Db 3137 CCAGTAGCTGACATTCATCCGGGGTCAGCACCGCTTTCTCGGACTTGGCTTTCTACGTGT 3196
QY 3571 TCTGGGTATACATTTAAGAAATCAGACTCGAGCAAGTCTAGAAAGCGCGCAAGATATC 3630
Db 3197 TCGCTTCTCTTTAGACCCCTTCGCGCCCTGAGTGTCTTGCGGACGCGTGAAGCTGTCAAT 3256
QY 3631 AAGGATCCACTAGCGTTAGAGCTCGCTGATCAGCCTCGACTGTGCTTC--TAGTTGCC 3688
Db 3257 CCGGTTAAATTTTGTAAATCAGCTCATTTTTTAAACCAATAGGCGGAAATCGGCAAA 3316
QY 3689 AGCATCTGTTGTTGCCCTCCCGTGGCTTCTTGACCCCTGGAGGTGCCACTCCCA 3748
Db 3317 TCCCTTATAAATCAAAAGATAGCCCGGATAGGCTGTGTTGTTCCAGTTTGGAAACA 3376
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QY 3809 TTCTGGGGGTGGGGTGGGCGAGCAGCAAGGGGAGGATTGGGAAGACAATAGCAGGC 3868
Db 3437 GCGATGGCGATCAGCTTATGCGGTGTGAATAACCCACAGATGCTTAAGGAGAAATAC 3496
QY 3869 ATCTGGGAGCTCTTCGCTTCTCGCTCAGTCACTGCTGCTGCGCTCGCTGCTGCTG 3928
Db 3497 CGCATCAGGGCTCTTCGCTTCTCGCTCAGTCACTGCTGCTGCGCTCGCTGCTGCTG 3556
QY 3929 CGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACGAATCAGGGAT 3988
Db 3557 CGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACGAATCAGGGAT 3616
QY 3989 AACGAGGAAGAACATGTGAGCAAAAGCGCAGCAAAAGCGCAGGAACCGTAAAAAGGCC 4048
Db 3617 AACGAGGAAGAACATGTGAGCAAAAGCGCAGCAAAAGCGCAGGAACCGTAAAAAGGCC 3676
QY 4049 GCGTTGCTGCGCTTTTTCATAGGCTCGGCCCGCTCGACGATCACAAAAATCAGCG 4108
Db 3677 GCGTTGCTGCGCTTTTTCATAGGCTCGGCCCGCTCGACGATCACAAAAATCAGCG 3736
QY 4109 TCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATACAGGCTTTTCCCTCTGGA 4168

Db 3737 TCAAGTCAGAGTGGGAAACCCGACAGACTATAAAGATACAGCGCTTTTCCCTCTGGA 3796
QY 4169 AGCTCCCTCGTGGCTCTCTGTTCCGACCTTCGCGCTTACCGGATACTGTCGCGCTTT 4228
Db 3797 AGCTCCCTCGTGGCTCTCTGTTCCGACCTTCGCGCTTACCGGATACTGTCGCGCTTT 3856
QY 4229 CTCCTTCCGGGAAGGTGGCGCTTTCTCAATCTCAGCTGCTAGGTATCTCAGTTCCGTTG 4288
Db 3857 CTCCTTCCGGGAAGGTGGCGCTTTCTCATAGCTACGCTGAGGTATCTCAGTTCCGTTG 3916
QY 4289 TAGGTCGTTCCGCTCAAGCTGGGCTGTGTGACGAAACCCCGCTTCAGGCCGACCTGC 4348
Db 3917 TAGGTCGTTCCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAGGCCGACCTGC 3976
QY 4349 GCTTATCCGGTAACATATCTGTTGAGTCCAAACCGGTAAGACACGATTTATGCCACTG 4408
Db 3977 GCTTATCCGGTAACATATCTGTTGAGTCCAAACCGGTAAGACACGACTTATGCCACTG 4036
QY 4409 GCAGCAGCACCTGGTAACAGGATTAGCAGAGCGAGTATGTAGGCGGTCTACAGAGTTC 4468
Db 4037 GCAGCAGCACCTGGTAACAGGATTAGCAGAGCGAGTATGTAGGCGGTCTACAGAGTTC 4096
QY 4469 TTGAAGTGGTGGCTTAACCTACCGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTG 4528
Db 4097 TTGAAGTGGTGGCTTAACCTACCGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTG 4156
QY 4529 CTGAAGCAGTATACCTTCGGAAAAAGTGTGTAGCTTTGATCCGGGCAAAACCAACACC 4588
Db 4157 CTGAAGCAGTATACCTTCGGAAAAAGTGTGTAGCTTTGATCCGGGCAAAACCAACACC 4216
QY 4589 GCTGTAGCGGTGTTTCTGTTGTCAGACGACAGATTACGCGCAAAAAAGGATCT 4648
Db 4217 GCTGTAGCGGTGTTTCTGTTGTCAGACGACAGATTACGCGCAAAAAAGGATCT 4275
QY 4649 CAAGAAGATCTTTGATCTTTCTACGG 4676
Db 4276 CAAGAAGATCTTTGATCTTTCTACTG 4303

RESULT 14

US-09-620-259-1
; Sequence 1, Application US/09620259
; Patent No. 6572881
; GENERAL INFORMATION:
; APPLICANT: Ronald Zuckermann et al.
; TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related
; Compositions and Methods Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,259
FILING DATE: 03-Oct-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1387.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

		LENGTH: 4328 base pairs			
		TYPE: nucleic acid			
		STRANDEDNESS: single			
		TOPOLOGY: linear			
		MOLECULE TYPE: DNA (genomic)			
		SEQUENCE DESCRIPTION: SEQ ID NO: 1:			
		US-09-620-259-1			
		Query Match			
		Best Local Similarity 36.8%; Score 2166.4; DB 4; Length 4328;			
		Matches 3060; Conservative 0; Mismatches 1236; Indels 52; Gaps 10;			
QY	333	GGGAATATTGGCTATTGGCCATTGCATAGCTGTGTATCTATATCAATAATGTACATTTA	392	TCCTTATGCTATAGGTGATGGTATAGCTTAGCCTATAGGTGGTATTGACCAATTATT	963
DB	4	GCGGAATTTTCGACTCTAGGCCATTGCATAGCTGTGTATCTATATCAATAATGTACATTTA	63	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1293
QY	393	TATTGGCTCATGTCCCAATATGACCGGCATGTGACATTTGATTTGACTAGTTATTAAATA	452	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1352
DB	64	TATTGGCTCATGTCCCAATATGACCGGCATGTGACATTTGATTTGACTAGTTATTAAATA	123	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1402
QY	453	GTAAATCAATTTACGGGGTCAATTAGTTTCATAGCCCATATATGAGAGTCCGGGTTACATAACT	512	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1462
DB	124	GTAAATCAATTTACGGGGTCAATTAGTTTCATAGCCCATATATGAGAGTCCGGGTTACATAACT	183	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1522
QY	513	TACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAAT	572	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1582
DB	184	TACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAAT	243	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1642
QY	573	GACGTATGTTCCCATAGTAAGCCCAATAGGGAATTTCATTTGACGTCAATGGGTGAGTA	632	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1702
DB	244	GACGTATGTTCCCATAGTAAGCCCAATAGGGAATTTCATTTGACGTCAATGGGTGAGTA	303	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1762
QY	633	TTTACCGTAACTGCCACCTTGGCGGTGATCAAGTGTATCATATGCGCAAGTCCGCCCCC	692	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1822
DB	304	TTTACCGTAACTGCCACCTTGGCGGTGATCAAGTGTATCATATGCGCAAGTCCGCCCCC	363	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1882
QY	693	TATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTACATGACCTTACG	752	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	1942
DB	364	TATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTACATGACCTTACG	423	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2002
QY	753	GGACTTTCTACTTGGCAGTACATCTACGTATTAGTATCGCTATTACCAATGTGATGCG	812	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2062
DB	424	GGACTTTCTACTTGGCAGTACATCTACGTATTAGTATCGCTATTACCAATGTGATGCG	483	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2122
QY	813	GTTTTGGCAGTACACCAATGGCGGTGATACCGGTTTGACTCACGGGATTTCCAAAGTCT	872	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2182
DB	484	GTTTTGGCAGTACACCAATGGCGGTGATACCGGTTTGACTCACGGGATTTCCAAAGTCT	543	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2242
QY	873	CCACCCCAATTGACGTCAATGGGAGTTGTTTGGCCACCAAAATCAACGGGACTTTCCAAA	932	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2302
DB	544	CCACCCCAATTGACGTCAATGGGAGTTGTTTGGCCACCAAAATCAACGGGACTTTCCAAA	603	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2362
QY	933	ATGTCGTATAAACCCCGCCCGTTGACGCAAAATGGCGGTGATGGCTGTACGGTGGAGGT	992	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2422
DB	604	ATGTCGTATAAACCCCGCCCGTTGACGCAAAATGGCGGTGATGGCTGTACGGTGGAGGT	663	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2482
QY	993	CTATATAAGCAGAGCTCGTTTGTAGTGAACCGTCAAGTCCGCTGAGACGCCATCCAGCTG	1052	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2542
DB	664	CTATATAAGCAGAGCTCGTTTGTAGTGAACCGTCAAGTCCGCTGAGACGCCATCCAGCTG	723	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2602
QY	1053	TTTGTGACCTCCATAGAAGACACCGGACCGGATCCAGCTCCGCGCGCGGAAACGGTGCAT	1112	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2662
DB	724	TTTGTGACCTCCATAGAAGACACCGGACCGGATCCAGCTCCGCGCGCGGAAACGGTGCAT	783	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2722
QY	1113	TGGAACCGGATTTCCCGTCCCAAGAGTGAAGTAAAGTACCGCTATAGACTCTATAGGCA	1172	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2782
DB	784	TGGAACCGGATTTCCCGTCCCAAGAGTGAAGTAAAGTACCGCTATAGACTCTATAGGCA	843	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2842
QY	1173	CACCCCTTTGGCTCTTATGATGCTACTACTGTTTGGCTTGGGCTTATACACCCCGC	1232	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2902
DB	844	CACCCCTTTGGCTCTTATGATGCTACTACTGTTTGGCTTGGGCTTATACACCCCGC	903	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	2962
QY	1233	TCCTTATGCTATAGGTGATGGTATAGCTTAGCTATAGGTGTTGAGCAATTATT	1292	GAACCACTCCCTATTGGTACAGCATCTTCCATTACTTAATCCATAAATGGCTCTTTGGCC	3022

Db 1957 CCGCGCTGGAGGATCATCCAGCGCGCTCCGCGAATAACGATTCGGAAGCCCAACCTTTC 2016
QY 2373 TGTGGGACTACCCCCCAAAACCTTGGGTATTTGTGCCGCGGAAGTGTGTGTGTCGG 2432
Db 2017 ATAGAAGCGCGGTGGAA-----TCGAAATCTGTATGCGCAGTTTGGGCGTCTGTGT 2072
QY 2433 GTATATTGCTTCACTCCAGCCCGGTGGTGGGAACGACGACAGGTCTGGCGCGCC 2492
Db 2073 CGGTCAATTTGCAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAGGGATAGAAGC 2132
QY 2493 ACCTACAGCTGGGGTGAATAATGATACGGAAGTCTTCGTCCTTAACAAATACCAAGCCACCG 2552
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QY 2553 CTGGGCAATTGTTGGTTGTACTGTGATGAATCAACTGTGATACCAAAAGTGTGCGGA 2612
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Db 2253 CACACCGAGCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCAATGAT--A 2310
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Db 2371 TTGAGCCTGGCAACAGTTTCGGTGGCGGAGCCCTGATGCTCTTTCGTCAGATCATCC 2430
QY 2793 ATATTAAATCAGGATGATGAGTGGAGGGGTGAAACACAGGCTGGAAGTGCCTGCAAC 2852
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QY 2853 TGAACGGGGCGAACTGTTCGATCTGGAAGATAGGGAAGTCCGAGATTCGATATGGAG 2912
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QY 2913 AACATACATCAGGAATTCATAGAACCTCTGCTCGTGTACAGCGGGGTTCCTGTTG 2972
Db 2545 GCCATATGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTCGCCCGGC 2604
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Db 2605 ACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGCAACGTCGAGCAAGCTGG 2664
QY 3033 GGGGATCTCCGCTGTCTTGGCCAAAATTCGAGTCCCAACCTCCCAATCACTCACCA 3092
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QY 3093 ACCTCTGTCTCGAATTTGTCTGTGTTATCGCTGGATGTCGCGGCTTTTATCAT 3152
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Db 2780 GCCGGAACACGGCGGCATCAGAGCAGCGATGTTCTGTTGTCGCCAGTCAATAGCCGA 2839
QY 3213 ATGTGCCCCCTTTGTCCTCTAATTCAGGATCAACCAACACAGTACGGGACCATGCAA 3272
Db 2840 GCCTCTCCACCAAGGGCGGAGAACCTGCGTGAATCCATCTGTTCAATCATGCGAA 2899
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Db 3017 CAGCTGGCAATTCGGTTCGCTTGTCTCCATAAACCGGCCAGTCTAGCTATCGCAATG 3076

QY 3453 TTCTGAGGCTTTCGCCCACTGTTGGCTTTCAGCTATATGATGATGTGTTATTTGGGG 3512
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QY 3631 AAGATCCACTAGCGGTAGAGCTCGCTGATCAGCTCGACTGCTGCTTC--TAGTTGCC 3688
Db 3257 CCGGTATAAATTTTGTAAATCAGCTCAATTTTAAACCAATAGGCCGAAATCGGCAAA 3316
QY 3689 AGCATCTGTTTGGCCCTCCCGTCCCTTCTGACCCCTGGAAGGTGCACCTCCCA 3748
Db 3317 TCCCTTAATAATCAAAAGNATAGCCCGAGATAGGTTGAGTGTGTTCCAGTTTGGAAACA 3376
QY 3749 CTGTCTTTCTAATAAATAGGAAATTCGATTCGATTTGTCAGTAGGTGTCAATCTA 3808
Db 3377 AGAGTCCACTATTAAAGAACGTGCACTCCAAAGTCAAAAGGGCGAAACCGCTATCAG 3436
QY 3809 TTTCTGGGGGTGGGTGGGCGAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGC 3868
Db 3437 GCGATGGCGGATCAGCTTATGCGGTGTAATACCGCACAGATGCTAGGAGAAATATC 3496
QY 3869 ATGCTGGGAGCTCTTCCGCTTCTCGCTCACTGCTCGCTCGCTCGGTCTGTTCCGGCTG 3928
Db 3497 CGCATCAGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGTCTGCTG 3556
QY 3929 CGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATTCACAGAAATCAGGGAT 3988
Db 3557 CGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATTCACAGAAATCAGGGAT 3616
QY 3989 AACGAGGAAGAACATGTGACAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAGGCC 4048
Db 3617 AACGAGGAAGAACATGTGACAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAGGCC 3676
QY 4049 GGGTGTCTGGCTTTTTCATAGGCTCCGCCCTTCCAGAGCATCAAAAAATCGACGC 4108
Db 3677 GGGTGTCTGGCTTTTTCATAGGCTCCGCCCTTCCAGAGCATCAAAAAATCGACGC 3736
QY 4109 TCAAGTCAAGGTGGGAAACCCGACAGACTATTAAGATAACAGCGTTTCCCTCTGGA 4168
Db 3737 TCAAGTCAAGGTGGGAAACCCGACAGACTATAAAGATACAGGCGTTTCCCTCTGGA 3796
QY 4169 AGCTCCCTGCTGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCTTT 4228
Db 3797 AGCTCCCTGCTGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCTTT 3856
QY 4229 CTCCCTTCCGGAAGCGTGGCTTTTCTCAATGCTCACTGCTAGTATCTCAGTTCGGTG 4288
Db 3857 CTCCCTTCCGGAAGCGTGGCTTTTCTCATAGTCACTGCTAGGTATCTCAGTTCGGTG 3916
QY 4289 TAGGTCTGCTCCTCAAGCTGGCTGTGTGACGAAACCCCGCTTACGCGCCGACCGCTGC 4348
Db 3917 TAGGTCTGCTCCTCAAGCTGGCTGTGTGACGAAACCCCGCTTACGCGCCGACCGCTGC 3976
QY 4349 GCCTTATCCGTAACCTATCTGTTGATCCAAACCGGTAAGACACCACTTATCGCCACTG 4408
Db 3977 GCCTTATCCGTAACCTATCTGTTGATCCAAACCGGTAAGACACCACTTATCGCCACTG 4036
QY 4409 GCAGCAGCCACTGTAACAGGATTTAGCAGAGGAGTATGTAGGCGGTGCTACAGAGTTC 4468
Db 4037 GCAGCAGCCACTGTAACAGGATTTAGCAGAGGAGTATGTAGGCGGTGCTACAGAGTTC 4096
QY 4469 TTGAAGTGTGGCTAACTACGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTG 4528
Db 4097 TTGAAGTGTGGCTAACTACGCTACACTAGAAAGGACAGTATTTGGTATCTGCGCTCTG 4156

Qy 4529 CTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACCAACC 4588
Db CTTAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACCAACC 4216
Qy 4589 GCTGGTAGCGGTGTTTCTTCTGTCGACGACGAGTTACGGCGCAGAAAAAGGATCT 4648
Db 4217 GCTGGTAGCGCGG-ITTTTGTGTCGACGACGAGTTACGGCGCAGAAAAAGGATCT 4275
Qy 4649 CAAGAAGATCCTTTGATCTTTCTACGG 4676
Db 4276 CAAGAAGATCCTTTGATCTTTCTACTG 4303

RESULT 15
US-08-799-569-1
; Sequence 1, Application US/08799569
; Patent No. 6133244
; GENERAL INFORMATION:
; APPLICANT: Michel, Marie-Louise
; APPLICANT: Mancine, Maryline
; TITLE OF INVENTION: Nucleotide Vector, Composition
; TITLE OF INVENTION: Containing Such Vector, and Vaccine for Immunization
; TITLE OF INVENTION: Against Hepatitis
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,569
; FILING DATE: 12-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/706,337
; FILING DATE: 27-APR-1994
; FILING DATE: 30-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/633,821
; FILING DATE: 22-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/00483
; FILING DATE: 27-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0128-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-799-569-1

Query Match 36.7%; Score 2156.6; DB 3; Length 5618;
Best Local Similarity 63.9%; Pred. No. 0;
Matches 3464; Conservative 0; Mismatches 1899; Indels 58; Gaps 11;
Qy 422 GTTGACATGATTAATGCTAGTATTATAAGTAATCAATACGGGTCAATAGTTCAATA 481
Db 232 GTTGACATGATTAATGCTAGTATTATAAGTAATCAATACGGGTCAATAGTTCAATA 291

Qy 482 GCCATATATGGAGTTCCGCGTTTACATAAATTACGGTAAATGGCCGCTGGCTGACCGC 541
Db GCCATATATGGAGTTCCGCGTTTACATAAATTACGGTAAATGGCCGCTGGCTGACCGC 351
Qy 542 CCAACGACCCCGCCCATTTGACGTCAATTAATGACGTATGTTCCCATAGTAACGCCAATAG 601
Db 352 CCAACGACCCCGCCCATTTGACGTCAATTAATGACGTATGTTCCCATAGTAACGCCAATAG 411
Qy 602 GGAATTTTCATTGACGTCAATGGTGGAGTATTACGGTAAATCTGCCACTTGGCGAGTAC 661
Db 412 GGAATTTTCATTGACGTCAATGGTGGAGTATTACGGTAAATCTGCCACTTGGCGAGTAC 471
Qy 662 ATCAAGTGTATCATATGCCAAGTCCGCGCCCTTATTGACGTCAATGACGGTAAATGGCCCG 721
Db 472 ATCAAGTGTATCATATGCCAAGTCCGCGCCCTTATTGACGTCAATGACGGTAAATGGCCCG 531
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Qy 782 TATTAGTCACTGCTATTACCATGGTGTGCGGTTTGGCAGTACACCAATGGCGGTGGAT 841
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Db 832 GAGAACCCACTGCTTAATCTGGCTTATCGAAAT--AATACGACTCACTATAGGAGACC 888
Qy 1082 GATCCAGCTCCGCGCGCGGAAACGGTGCATTGGAAACGGGATTCGCCGTCGCAAGAGTG 1141
Db 889 CAAGCTTGGTAGCGGGCCCCCTCGAGGATTTGGG-----ACCCCTCGCTGAACA 939
Qy 1142 AGTAAGTACGCTTATAGACTCTATAGCACAACCCCTTTGGCTCTTATGCTATATAC 1201
Db 940 TGGAGAACATCATCAGGATTCCTAGG----ACCCCTTCTCGTGTACAGCGGGGTTT 995
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Qy 1382 ACTCTGCTCTCAGAGACTGACACGGACTCTGTAT--TTTTACAGGATGGGTCCATTTAT 1440
Db 1176 TTTATCATCTTCTCTTCTCTGCTGCTATGCTCATCTTCTTGTGGTCTTCTCTGGAC 1235
Qy 1441 TATTTACAAATTCATATATAACAACACCGCTCCCGCGCGCAGTGTTTTATTAACA 1500
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Qy	1561	GGCGGAGCTTCCACATCGGAGCCCTGTGTCCATCCGTCTCAGCGGCTCATGGTGTGCTCGGC	1620
Db	1356	ACCAAACTTTGGGACGGAAATTGCACCTGTATTTCCCATCCCATCATCTCTGGGCTTTGGGA	1415
Qy	1621	AGCTCCCTTGCTCCTTAACAGTGGAGGCGCAGACTTAGGCACAGCAAAATGCCCCACCAACC	1680
Db	1416	AAATTCCTATATGGGAGTGGGCGCTCAGCCCGTTTCTCTGGCTCAGTTTACTAGTGGCATT	1475
Qy	1681	AGTGTGCGCGCAAAAG-----CGTGGCGGTAGGGTATGTGTCTGAAATAGAGCTCGGA	1734
Db	1476	GTTTCAGTGGTTTCGTPAGGGCTTTCCCCCACTGTTTGGCTTTTCAGTTATATGATGATGTGG	1535
Qy	1735	GATTGGGCTCGACCTCGAGCGAGATGGAAGACTTAAGGCGAGCGGCAAGAAGAAGATGCAG	1794
Db	1536	TATTGGGGGCGCAAGTCTGTACAGCATCTTGAGTCCCTTTTTTACCGCTGTTTACCAATTTTC	1595
Qy	1795	GCAGCTCAGTGTGTGTAATTCGTATAAGATCAGAGGTAACTCCCGTTTGGGTGCGGTGCTGTAA	1854
Db	1596	TTTTGTCTTTTGGGTATACATTTAAACCCCTAACAAAAACAAGAGATGGGGTTACTCTCTAA	1655
Qy	1855	CGGTGGAGGCGAGTGTAGTCTGAGCAGTACTCGTTGTCTGCGGCGCGCCACCAGACATA	1914
Db	1656	ATTTTATGGGTATGTCTCATTTGGTATTTAGGTCCTTCCACAAGAACAATATACATAAA	1715
Qy	1915	ATAGCTACAGACTAACAGACTGTTCCTTCCATGGGTCTTTTCTGCAGTCAACGTGCTG	1974
Db	1716	AAATCAAAAGAAATGTTTTAGAAAACTTCTCTATTACAGGCTTATTTGATTGAAAGTATGTC	1775
Qy	1975	GACCAATTCAGCAATCATGTGATGCATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGT	2034
Db	1776	AACGAAATGTGGGTCTTTTGGGTTTTGTGCTGCCCTTTTACAAATGTGTTTATCTCTGCGT	1835
Qy	2035	GTGGAGCAGTCTTCGTTTCGCCAGCTAGCGAAAAACCACGTCAACGGGGGAAGTGCCG	2094
Db	1836	TGATGCCCTTTGTATGATGTATTCAATCTAAGCAGGCTTTTCACTTCTCGCCAACTTACA	1895
Qy	2095	GCCACATGTGTCTGGAATTTGTAGCCTCTCTGCACCAAGCGGCCCAAGCAAAAGTCCAGC	2154
Db	1896	AGGCTTCTCTGTGTAAACAATACCTGAAACCTTTACCCCGTTGCCGCCAACGCCAGGTC	1955
Qy	2155	TGATCAACCAACGCGGAGTTGGCACCTCAATAGCACGGCCCTGTGAATGCAATGATAGCC	2214
Db	1956	TGTGCCAAGTGTTTGTCTGACGCAACCCCACTGCTGCGGCTTGTGTCATGGGCCATCAGC	2015
Qy	2215	TCAACACCGCTGTGTGGCAGGCTTTTCTATACCACAAAGTTCAACTTCTCAGGCTGTC	2274
Db	2016	GCATGCGTGGAACTTTTTCGGTCTCTCTCGGATCTCATCTGCGGAACCTCTAGCCGCTT	2075
Qy	2275	CTGAGGGCTAGCCAGCTGCGGACCCCTTACCGATTTTGACAGGGCTGGGGCCCTATCA	2334
Db	2076	GTTTTGTCTGCAGCAGTCTGG-----AGCAAAACATTTACGGACTGATAACTCTGTT	2128
Qy	2335	GTTATGCCAAGGAGCGGCCCGACAGCGCCCTACTGCTGGCACTACCCGCCAAAAC	2394
Db	2129	GTCCTATCCGCGAAATATACATCGTTTTCATGGCTGTAGGCTGTGCTGCCAATCGGATC	2188
Qy	2395	CTTTCGGTATTGTGCCCGCGAAGAGTGTGTGTGTCGGGTATATGCTTCACTCCCAAGCC	2454
Db	2189	CTGCGCGGACGTCTTTTGTATTAGTCCCGTCGCGCTGAACTCTGCGGACGACCCCTTCT	2248
Qy	2455	CCGTGTGTGGGAACACCGACAGGTCTGGGCGCGCCCACTACAGCTGGGGGTGAAAATG	2514
Db	2249	CGGGGTGCTGGGAC-----TCTCTGTCCTTCTCCGTCTGCGTTCGACCC	2298
Qy	2515	ATACGGAAGTCTTCGTCTTTAACAATACAGGCCACCGCTGGGCAATTGGTTGTGGTTGTA	2574
Db	2299	GACCACGGGGCGCACCTCTCTTTACGGGGAATCCCGCTCTGTGCTCTCTCATCTGCGGA	2358
Qy	2575	CCTGGATGAACCTCAACTGGATTACCAAGTGTGCGGAGCGCTCTCTGTGTGTCATCGGAG	2634
Db	2359	CCGTGTGCATCTCGCTTCACTCTGACAGTGCATATGGAGACCAACCGTGAACGCCCAAC	2418
Qy	2635	GGGCGGGCAACAAACACCTGTCACTGCCCCCACTGATTGCTTCCGCAAGCATCTCGGACGCCA	2694

Db	2419	ATATGCCCAAGGTCCTTACATAAAGAGGACTCTTGGACTCTCAGCAATGTCAACGACCGAC	2478
Qy	2695	CATACTCTCGGTCCGGTCCCGTCCCGATCACACCCAGGTGCCTGTGTCGACTACCCGT	2754
Db	2479	CTTGAGGCATACCTTCAAAGACTGTTTGTAAAGACTGGAGGATTTGGGGAGGAGATT	2538
Qy	2755	ATAGGCTTTGGCATTATCCTTGTACATCAACTACACCATATTTAAATACAGATGTACG	2814
Db	2539	AGGTTAAAGGTCTTTTGTACTAGGAGCTGTAGSCATAAAATTTGGTCTGCGCACAGCACCA	2598
Qy	2815	TGGAGGGGTGGAACACAGGCTGGAAGCTGCCTGCAACTGAGCGGGGCGAACGTTGCG	2874
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Qy	2875	ATCTGGAAGATAGGGACAGGTCGAGATCGATATGGAGAACATCATCAGGATTCCTAG	2934
Db	2659	AGCTGTGCCTTGGTGGCTTTGGGGCATGGACATCGACCTTATAAAGAAATTTGGAGCTA	2718
Qy	2935	GACCCCTGCTCGTGTACAGGGGGGTTTTTCTTGTGTGACAAAGAACTCTCACAAATACCGC	2994
Db	2719	CTGTGGAGTTACTCTCGTTTTTGGCCTTCTGACTTCTTCTCAGTACGAGATCTGGCCA	2778
Qy	2995	AGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGATCTCCCGTGTCTTTCG	3054
Db	2779	GGATCCACTAGTTCTAGAGCGCGCCACCGCGTGGAGCTCCAGCTTTTGTTCCTTTTA	2838
Qy	3055	GCCAAATTCGCGAGTCCCAACCTCCAACTCACTCAACCACTCTCTCTCTCCAAATTTGTC	3114
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Qy	3115	CTGGTTATCGCTGGATGTGTCTGCGCGGTTTTATCATATTCCTCTTTCATCTCTGCTCTAT	3174
Db	2899	CTGCTTTGCCGAATCATGCTGGAATAAGCGGCTTTTCTGGATTCATCGACTGTGGCCG	2958
Qy	3175	GCCTCATCTTCTATTGTTTCTCTGGATATCAAGGTATGTTGCCGTTTGTCTCTCTAA	3234
Db	2959	GCTGGGTGTGGCGGACCGCTATCAGACATAGCGTTTGGCTCCCGTGATATTGCTGGAAG	3018
Qy	3235	TTCCAGGATCAACAAACAGTACGGGACCATGCAAAACCTGACAGACTCTCTGTCTCAAG	3294
Db	3019	GCTTGGGGGAATGGCTGACCGCTTCTCTGTCTTTAAGGTATCGCGTCCCGATTTC	3078
Qy	3295	GCAACTCTATGTTTCCCTCATGTTGTGTGTAACAAACCTACGATGGAATTCACCTGTA	3354
Db	3079	GCAGCGCATCGCCTCTATCGCCTCTTTCAGCAGTCTTCTTGAGCGGACTCTGGGGTTC	3138
Qy	3355	TTCCCATCCCATCGTCTGGGCTTTCGAAAAATACCTATGGGAGTGGGCTCAGTCCGTT	3414
Db	3139	GAATGACCGACCAACGACGCCCACCTGCCATCACGAGATTTTCGATTTCCACCGCGCC	3198
Qy	3415	TCTCTTGGCTCAGTTACTTAGTSCCATTTGTTTCAGTGGTTCTGTAGGGCTTTCGCCACATG	3474
Db	3199	TTCTATGAAAGTTGGGCTTCGGAATCGTTTTTCGGGACGCGGCTGGATGATCTCCAG	3258
Qy	3475	TTTTGGCTTTCAGCTATATGATGATGTGTTATTTGGGGGCAAGTCTGTACAGCATCGTGA	3534
Db	3259	CGCGGGGATCTCATGCTGGAGTCTTCGCCCAACCTTGTGTTATTCAGCTTATAAT	3318
Qy	3535	GTCCCTTTTACCGCTGTGTACCAATTTTCTTTGTCTCTGGGTATACATTTAAGAATTCA	3594
Db	3319	GGTTACAAATAAAGCA-ATAGATCACAAAATTTCAAAATAAAGCAATTTTTTTCATGCA	3377
Qy	3595	GACTCGAGCAGCTAGAAAGGCGCCAGATATC- - -AAGGATCCACTACGGGTTAG	3650
Db	3378	TTCTAGTTGTGGTTTGTCCAAACTCATCAATGATGTTATCTATCTGTCTGGATCCCGTCGAC	3437
Qy	3651	AGCTCGTGAATCAGCCTCGACTGTGCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCCTC	3710
Db	3438	CTCGAGAGCTTGGCGTAACTCATGGTCTAGCTGTTTCTCTGTGGAATTTGTTATCCGCTC	3497
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Qy 3771 GGAAATTCGATCGCATTTCTGAGTAGGTGTCAATTTCTATTTCTGGGGGTGGGGTGG ---G 3827
Db 3558 GTGAGCTAACTCAATTAATTGGCTTGGCTCACTGCCCGCTTCCAGTTCGGGAAACCTG 3617
Qy 3928 GCAGGACAGCAGAGGGGAGAGATTGGGAAGACAATAGCAGGCATGC-----TGGGG 3877
Db 3618 TCGTGCCAGCTGCAATTAATGAATCGGCCAAACCGCGCGGAGAGCGGTTTGGCGTATTGGG 3677
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Db 3678 CGCTTTTCGCTTCCGCTTCCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCGAGCG 3737
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Qy 3998 AAGAAATGTAGCAAAAGCCAGCAAAAGCCAGGAACCGTTAAAGAGCGCGGTTCGCTG 4057
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Qy 5798 CGAAAAAGTCCACCTGACGTC 5818
Db 5598 CGAAAAAGTCCACCTGACGTC 5618

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Job time : 1097 secs

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2005, 05:45:13 ; Search time 3019 Seconds
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11860.806 Million cell updates/sec

Title: US-10-715-665-6

Perfect score: 5882

Sequence: 1 tcgcgcgttcgtgatgac.....tatcacgagcccttcgctc 5882

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2654.4	45.1	10263	18	US-10-609-019-2
2	2419.2	41.1	6236	18	US-10-491-121-41
3	2397.8	40.8	6050	17	US-09-491-974-4
4	2397.8	40.8	6050	17	US-10-394-388A-4
5	2395.6	40.7	6148	18	US-10-491-121-24
6	2363	40.2	6258	18	US-10-491-121-34
7	2331	39.6	7685	19	US-10-763-976A-14
8	2321.4	39.5	7626	17	US-10-401-000-2
9	2311.8	39.3	7617	17	US-10-401-000-1
10	2290.6	38.9	6577	17	US-10-359-120-50
11	2283.4	38.8	6505	17	US-10-359-120-15
					Sequence 2, Appli
					Sequence 41, Appl
					Sequence 4, Appli
					Sequence 24, Appl
					Sequence 34, Appl
					Sequence 14, Appl
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 50, Appl
					Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-10-609-019-2

; Sequence 2, Application US/10609019

; Publication No. US20040197910A1

; GENERAL INFORMATION:

; APPLICANT: Cooper, Richard K.

; APPLICANT: Cadd, Gary G.

; APPLICANT: Fioretti, William C.

; APPLICANT: DeBoer, Kenneth F.

; TITLE OF INVENTION: Gene Regulation in Transgenic Animals Using a Transposon-Based

; FILE OF INVENTION: Vector

; FILE REFERENCE: 51687-0101 (51687-287015)

; CURRENT APPLICATION NUMBER: US/10/609,019

; CURRENT FILING DATE: 2003-06-26

; PRIOR APPLICATION NUMBER: US 60/392,415

; PRIOR FILING DATE: 2002-06-26

; PRIOR APPLICATION NUMBER: US 60/441,392

; PRIOR FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: US 60/441,377

; PRIOR FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: US 60/441,502

; PRIOR FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: US 60/441,405

; PRIOR FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: US 60/441,447

; PRIOR FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: US 60/441,381

; PRIOR FILING DATE: 2003-01-21

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 10263

; TYPE: DNA

; ORGANISM: Artificial Sequence

Sequence 34, Appli

Sequence 51, Appl

Sequence 157, App

Sequence 32, Appl

Sequence 100, App

Sequence 8, Appli

Sequence 158, App

Sequence 105, App

Sequence 106, App

Sequence 33, Appl

Sequence 122, App

Sequence 103, App

Sequence 84, Appl

Sequence 107, App

Sequence 16, App

Sequence 1, Appli

Sequence 1, Appli

Sequence 115, App

Sequence 3, Appli

Sequence 4, Appli

Sequence 144, App

Sequence 130, App

Sequence 145, App

Sequence 128, App

Sequence 114, App

Sequence 108, App

Sequence 99, Appl

Sequence 67, Appl

Sequence 10, Appl

Sequence 116, App

Sequence 101, App

Sequence 29, Appl

Sequence 31, Appl

; FEATURE:			
; OTHER INFORMATION: Synthetic			
US-10-609-019-2			
Query Match 45.1%; Score 2654.4; DB 18; Length 10263;			
Best Local Similarity 69.5%; Pred. No. 0;			
Matches 4315; Conservative 0; Mismatches 1156; Indels 737; Gaps 23;			
QY	340	ATTGGCTATTGGCATTGCAATGACATGCTGATCTATATCATATAATATGACATTTATATGGC	399
DB	4056	ATTGGCTATTGGCATTGCAATGACATGCTGATCCATATCATATAATATGACATTTATATGGC	4115
QY	400	TCATGTCCATATAGCGCCATGCTTGACATTGATTTAGCTAGTTATTAATAGTAAATCA	459
DB	4116	TCATGTCCATATAGCGCCATGCTTGACATTGATTTAGCTAGTTATTAATAGTAAATCA	4175
QY	460	ATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGGCTTACATAACTTACGGTA	519
DB	4176	ATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGGCTTACATAACTTACGGTA	4235
QY	520	AATGGCCCGCTGGCTGACCGGCCAACAGACCCCGGCCATTGACGTCATTAATGACGTAT	579
DB	4236	AATGGCCCGCTGGCTGACCGGCCAACAGACCCCGGCCATTGACGTCATTAATGACGTAT	4295
QY	580	GTTCCTCATAGTACGCCAATAGGACTTTCCATTGAGGTCMAATGGGTGGAGTATTTACGG	639
DB	4296	GTTCCTCATAGTACGCCAATAGGACTTTCCATTGAGGTCMAATGGGTGGAGTATTTACGG	4355
QY	640	TAAACTGCCACATTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCTATTGAC	699
DB	4356	TAAACTGCCACATTTGGCAGTACATCAAGTGTATCATATGCCAAGTAGGCCCTATTGAC	4415
QY	700	GTCAATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTACATGACCTTACGGGACTTT	759
DB	4416	GTCAATGACGGTAAATGGCCCGCTGGCATTTATGCCAGTACATGACCTTATGGGACTTT	4475
QY	760	CCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGGCTTTGG	819
DB	4476	CCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGGCTTTGG	4535
QY	820	CAGTACACCAATGGGCGTGATAGCGGTTTGAATCTACCGGGGATTTCCAAAGTCTTCCACCCC	879
DB	4536	CAGTACATCAATGGGCGTGATAGCGGTTTGAATCTACCGGGGATTTCCAAAGTCTTCCACCCC	4595
QY	880	ATTGACGTCAATGGGAGTTTGTGTTGGCCACCAAAATCAACGGGACTTTCCAAATGCTGT	939
DB	4596	ATTGACGTCAATGGGAGTTTGTGTTGGCCACCAAAATCAACGGGACTTTCCAAATGCTGT	4655
QY	940	AATAACCCCGCCCGTTGACGCAAAATGGGCGGTAGGCGGTACGGTGGGAGGTCATATA	999
DB	4656	AACAACTCCGCCCATTTGACGCAAAATGGGCGGTAGGCGGTACGGTGGGAGGTCATATA	4715
QY	1000	AGCAGAGCTCGTTTGTAGTGAACCGTTCAGATCGCTCGGAGAGCGCCATCCACGCTGTTTGGAC	1059
DB	4716	AGCAGAGCTCGTTTGTAGTGAACCGTTCAGATCGCTCGGAGAGCGCCATCCACGCTGTTTGGAC	4775
QY	1060	CTCCATAGAAGACACCGGAGCCGATCCAGCTCCGCGCGGGGAAACGGTGCATTTGAAACG	1119
DB	4776	CTCCATAGAAGACACCGGAGCCGATCCAGCTCCGCGCGGGGAAACGGTGCATTTGAAACG	4835
QY	1120	CGGATTTCCCGTCCCAAGAGTACGTAAAGTACCGCTATAGCTCTATAGGCACACCCCT	1179
DB	4836	CGGATTTCCCGTCCCAAGAGTACGTAAAGTACCGCTATAGCTCTATAGGCACACCCCT	4895
QY	1180	TTGGCTCTTATGATGCTATCTGTTTGGCTTTGGGCGCTATACACCCCGC-TCCTTTA	1238
DB	4896	TTGGCTCTTATGATGCTATCTGTTTGGCTTTGGGCGCTATACACCCCGCTTCTTTA	4955
QY	1239	TGCTATAGGTGATGATAGCTTAGCTATAGGTGTTGGGTATATGACCACTTATTTGACAC	1298
DB	4956	TGCTATAGGTGATGATAGCTTAGCTATAGGTGTTGGGTATATGACCACTTATTTGACAC	5015
QY	1299	TCCCTTATTGGTGACGATCTTTCCATTACTTAATCCATAACATGGGCTCTTTGGCCAACT	1358
DB			

5016	TCCCTTATTGGTGACGATACTTTCCATTACTAATCAATACATGGCTCTTTGGCCAACT	5075
1359	ATCTCTATTGGCTATATGCAATACTCTCTCTTACAGAGACTGACACGGACTCTGTATTTT	1418
5076	ATCTCTATTGGCTATATGCAATACTCTCTCTTACAGAGACTGACACGGACTCTGTATTTT	5135
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5136	TTACAGGATGGGGTCCCAITTTATTATTACAAATTCACATATACAAACACGCGCTCCCCC	5195
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5196	GTGCCCGCAGTTTATTATTAAACATAGCGTGGGATCTCCACGGCAATCTCGGGTACGTGTT	5255
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5256	CCGGACATCGGGCTCTTCTCCGGTAGCGCGGAGCTTCCACATCCGAGCCCTGGTCCCATG	5315
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5316	CTTCCAGCGGCTCATGGTCTCGCGAGCTCTTGTCTCTTAACAGTGGAGGCCAGACTTA	5375
1655	GGCAGACACAATGCCACACACAGTGTGCGCACAAAGCCGCTGGCGGTAGGGTATG	1714
5376	GGCAGACACAATGCCACACAGTGTGCGCACAAAGCCGCTGGCGGTAGGGTATG	5435
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5436	TGTCTGAAATGAGCTCGGAGATTGGGCTCGCACGCCTGACGAGATGGAAGACTTAAAGG	5495
1774	CAGCGCGAAGAAGATGACAGGAGCTGAGTTGTTGTATTCTGATTAAGAGTACAGGTTAA	1833
5496	CAGCGCGAAGAAGATGACAGGAGCTGAGTTGTTGTATTCTGATTAAGAGTACAGGTTAA	5555
1834	CTCCGTTTCCGGTGTCTTAAACGCTGGAGGAGTGTCTGAGCAGTACTCGTTGCTG	1893
5556	CTCCGTTTCCGGTGTCTTAAACGCTGGAGGAGTGTCTGAGCAGTACTCGTTGCTG	5615
1894	CGCGCGCGCCACACAGACATAATAGCTGACAGACTAAACAGACTGTTTCCATCGGTC	1953
5616	CGCGCGCGCCACACAGACATAATAGCTGACAGACTAAACAGACTGTTTCCATCGGTC	5675
1954	TTTTCTGAGTCAACCGTGC-----	1972
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1973	-----TCGACGAATTCAGCAATCATGGATGCA-----	2000
5736	CAAGAAGCTCATCAGGAGTTTATGGCTTCAAGGTGCGCATGGAGGGCACCGTGAACGG	5795
2001	-----ATCAAGAGAGGCTCTGCTGTGTGCTGCTGTGTGTGGAGAGCTTTCGTT	2051
5796	CCACGAGTTTCGAGATCGAGGGCGAGGGCGAGGGCGGCCCTACAGAGGGCCACAAACCGT	5855
2052	TGCCCAGCGCTAGCGAAACCCACGTCAACGGGGGAGTGCAGGCCACACTGTGTGGA	2111
5856	GAAGCTGAAGAGTCAACAGGGCGGCCCTGCTGCTGCGCTGGGACATCTGTGCCCCCA	5915
2112	TTTTGTTAGCC-----	2121
5916	GTTCGAGTACGGCTCCAGGTGTACGTGAAGCAACCCCGCGGACATCCCGACTACAAGAA	5975
2122	-----TCCTCGCACCGAGCGCCAGAGAACGTCAGCTGATCAACACAAACGGCAGTTG	2176
5976	GCTGTCTTCCCGAGGGCTTCAAGTGGGAGCGCGTGTATGAATTCGAGGAGCGCGCGCT	6035
2177	GCACCTCAATAGCAAGCGCCCTGAACTGCAATGATAGCTCAACACCGGCTGTGTGAGG	2236
6036	GGTGAACCGTGAACCGGAGCTCTCTCCCTGAGGACCGCTCTTCTCATCTACAAGGTGAAGTT	6095
2237	GCTTTTCTATACCAACAGTTTCAATCTTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCCG	2296

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Qy 2297 ACCCTTACCGATTTTGACAGGGCTGGGGCCCTATCAGTTATGCCAAACGAAAGCGGCC 2356
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Qy 2357 CGACAGCGCCCTACTGCTGGCACTACC-----CCCCAA 2391
Dd 6216 CCGAAGCTGAAGACGCGCGCCACTACTGCTGGAGTTCAAAGTCCATCTACATGGCCAA 6275
Qy 2392 AACCTTCGGTATTTGCGCGGAGAGTGTGTGCTCGGTATATGCTTCACTCCC- 2450
Dd 6276 GAAGCCCGTGAAGTGTGCGCGCTACTACTAGTGGACTCCAAGCTGACATCACTCCCA 6335
Qy 2451 -----AGCCCGTGTGTGGGAACGACCGACAGTCCGGGCGCCCACTACA 2499
Dd 6336 CAACGAGGACTACACCATCTGGAGCAGTAGAGGCGACCGAGGCGCCCACTCTGTT 6395
Qy 2500 GCTGGGTGAAATGA-----TACGAGCTTTCGT 2530
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Dd 6816 TAGCGAAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCTGAAATGCGGAATG 6875
Qy 2898 GAGATCGATATGAGAACATCAGATCAGGATTCCTAGGACCCCTGCTGTTACAGGCG 2957
Dd 6876 GAAATGTAGGTTAATATTTTGTTHAAATTCGCTTAAATTTTGTTHAAATCAGCTCA 6935
Qy 2958 GGGTTTTTCTGTGCAAGAATCCTCACAAATCCG----- 2993
Dd 6936 TTTTAAACCAATAGGCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGACCGAG 6995
Qy 2994 -----CAGAGCTAGACTCGTGGTGGCACTTCTCTC 3023
Dd 6996 ATAGGGTTGAGTGTGTTCAGTTTGGAAACAAGATCCACTATTAAGAAACGTGGACTCC 7055
Qy 3024 AATTTCTAGGGGATCTCCCGTGTCTTGGCCA----- 3058
Dd 7056 AACGTCAAAGGGGAAACCGTCTATCAGGGCGATGGCCCACTACTCCGGGATCATATG 7115
Qy 3059 ----- 3058
Dd 7116 ACAAGATGTATCCACTTAACTTAATGATTTTACAAATCAATTAGGGGATTCATCA 7175
Qy 3059 ----- 3058
Dd 7176 GTGCTCAGGGTCAACGAGAAATAACATTCGGTCAGGAAAGCTTATGATGATGATGTGCTT 7235

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Dd 7236 AAAAACTTACTCAATGGCTGGTTATGCATATCGCAATACATCGAAAAAACAATAAGAGC 7295
Qy 3098 CTGCTCTCCAAATTTGCTGGTTATCGCTGGATGTGTCTGCGGGCTTT----- 3145
Dd 7296 TTCCGATAAAAAAGGCCAATTTATGCTATTTACCGCGCTTTTATTGAGCTTGAAG 7355
Qy 3146 -----TATCATATTCCTTCTTCACTCCCTGCTGCTATGCTCATCTTCTT 3187
Dd 7356 AATAATAAATAGATAGGTTTATTTGAAGCTAAATCTTCTTATCGTAAAAAATGCCCT 7415
Qy 3188 ATTGGTTCTTCTGGAATTAACAAGTATGTGCCCG----- 3222
Dd 7416 CTTGGGTATCAAGAGGCTATATATTTCCGCGAATAACATCATTTGGTGACAAATAA 7475
Qy 3223 ----- 3222
Dd 7476 CTAAGCACTTGTCTCTGTTTACTCCCTGAGCTTGAGGGTTAAACATGAAGGTCACTGA 7535
Qy 3223 -----T 3223
Dd 7536 TAGCAGATAATAATACGTAAAAACGCTAAACCAATAATCAAAATCCAGCCATCCCAAT 7595
Qy 3224 TTGCTCTCTAAATTCAGGATCAACAACACAGTACGGACCATGCAAAACCTGCACGAC 3283
Dd 7596 TGGTAGTGAATGATTAATAACAGCAACAGTAAATGGCCAAATACACCGGTTGATTT 7655
Qy 3284 TCCTGCTCAAGCAACTCTATGTTTCCCTCATGTGCTG----- 3322
Dd 7656 GGTAGGCTCACCAATAATCCCTGTAAAGCACCTTGTGATGACTCTTTTGGATAGA 7715
Qy 3323 -----TACAAAACCTACGATGGAATTTGCACCTG 3352
Dd 7716 CATCACTCCCTGPAATGCAAGTAAAGCATGCCACCAAGCAATAAATAAACAAG 7775
Qy 3353 TATTCCTCATCCATCGCTCGGCTTTTCGCAAAATACCTATGGAGTGGGCCCTCAGTCCG 3412
Dd 7776 GAAACTACCAACCTTCAGATATAAACGTAAGGCAATGCACTACTATCTGCAT 7835
Qy 3413 TTTCTCTTGGCTCAGTTTACTAGTGCATTTGTTTCAGTGGTTCGTAGGGCTTTCCGCCAC 3472
Dd 7836 AAATCCGAGCAGTACTCGCGTTTTCGCCCCATTTAGTGGCTATCTCTCGCACAAAG 7895
Qy 3473 TGTTCGCTTTCAGCTATA-----TGGATGATGTTGTTATGGGGGCCAAG-----TCTGT 3522
Dd 7896 GCTTGAATACTGAGTGTAAAGACCAAGACCCGTAATGAAAGCCCAACCATCATGCTAT 7955
Qy 3523 ACAGCATCGTACCTCTTATACCGCTGTACCAATTTTCTTGTCTCTGGGTATACA 3582
Dd 7956 TCATCATCAGATTTCTGTAAATAGCACACACCGTCTGGATTCGCTATCAATCGCTGA 8015
Qy 3583 TTTAAGAATTCAGACTCGAGCAAGTCTAGAAAGCGCGCAAGATATCAAGATCCACTA 3642
Dd 8016 AATAATAACAATAATGCGATCGTTAAATAGTATGATATACCGATCAGCTTTTGTTC 8075
Qy 3643 CGGTTAGAGCTCGTATCAGCTCGAC-----TGTGCTTCTAGTTGCCAGCCATC 3695
Dd 8076 CTTTAGTGAAGGTTAATTCGCGCTTGGCGTAATCATGTCATAGCTGTTTCTGTGTGA 8135
Qy 3696 TGTGTTTTCGCTCCCGCTGCTTCTTACCTTCGAGCCCTGGAAGGTGCCATCCCACTGCTCT 3755
Dd 8136 AATTGTTATCCGCTCAATTCACACATACAGAGCCGGAAGCATAAAGTGAAGCC 8195
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Dd 8196 TGGGGTGCCTAATGAGTGAAGTCACTAAATTTGCGTTGGCTCACTGCCCGCTTC 8255
Qy 3816 GGGTGGG---TGGGGCAGACAGGAGGGGAGGATTTGGGAAGACAATAGAGGATGC 3872
Dd 8256 CAGTCGGGAAACCTGTCGTGCCAGTGCATTAATGAATCGGCCAACCGCGGGGAGAGGC 8315

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Qy	3983	GGGGATAACGCAGGAAAGAAATCTGAGCAAAAGCCAGCAAAAGGCCAGGAACCGTAAA	4042
Db	8436	GGGGATAACGCAGGAAAGAAATCTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA	8495
Qy	4043	AAGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTTACAGAGCATCAAAAAAT	4102
Db	8496	AAGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTTACAGAGCATCAAAAAAT	8555
Qy	4103	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACACAGGCGTTTCCC	4162
Db	8556	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACACAGGCGTTTCCC	8615
Qy	4163	CCTGGAAAGCTCCCTGCTGCGCTCTCTGTTTCCGACCTGCGGCTTACCGGATACCTGTCC	4222
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Db	8676	GCCTTCTCCCTTCGGGAAAGGTGGCGCTTTCTCAATGCTCAGCCTGATGGTATCTCAGT	8735
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Db	8736	TCGGTGTAGTGCTGTTCCGCTCCAAGCTGGGCTGTGTGACAGAAACCCCGGTTACGCCGAC	8795
Qy	4343	CGCTGCGCCTTATCCCGGTAACTATCGTCTTGAGTCCAACCGGTAAACACACGACTTATCG	4402
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Qy	4643	GGATCTCAAGAAGATCCTTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGACGAAAC	4702
Db	9096	GGATCTCAAGAAGATCCTTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGACGAAAC	9155
Qy	4703	TCAAGTTAAAGGATTTTGGTCATCAGATTAATCAAAAAGGATCTTCACCTAGATCCCTTTA	4762
Db	9156	TCAAGTTAAAGGATTTTGGTCATCAGATTAATCAAAAAGGATCTTCACCTAGATCCCTTTA	9215
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Db	9276	TACCAATGCTTAATCAGTGAGGCAACCTATCTCAGCGATCTGTCTATTTGTTTCATTCATTA	9335
Qy	4883	GTTGCCCTGACTCCCGCTGCTGATGAATCACTACGATACGGAGGGCTTACCATCTGGCCCC	4942
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Qy	4943	AGTGCTGCAATGATACCGCGAGACCCACGGCTCACCGGCTCCAGATTTTATCAGCAATAAAC	5002

RESULT 2

US-10-491-121-41

US-10-491-121-41
: Sequence 41, Application US/10491121; sequence 41, Application 03/195
: Publication No. US20040259825A1; PUBLICATION NO: US20
: GENERAL INFORMATION:
: GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: NABEL, GARY

; APPLICANT: NABEL, GARY
; APPLICANT: YANG, ZHI-YONG

; APPLICANT: YANG, ZHI-YONG
: APPLICANT: SUI-I-TVAN, NANCY

APPLICANT: SULLIVAN, NANCY
APPLICANT: SANCHEZ, ANTHONY

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TITLE OF INVENTION: Development of a Preventive Vaccine for

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; TITLE OF INVENTION: FLOWVIR
FILE REFERENCE: NTH221 001ND

FILE REFERENCE: NIH221.001NP
CURRENT APPLICATION NUMBER: US/10/491 121

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; PRIOR APPLICATION NUMBER: PCT/US02/30251
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/326476
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 6236
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct pVR1012x/s Laasa (codon optimized)
us-10-491-121-41

Query Match 41.1%; Score 2419,2; DB 18; Length 6236;
Best Local Similarity 70.9%; Pred. No. 0;
Matches 3491; Conservative 0; Mismatches 1298; Indels 133; Gaps 16;

QY 1 TCOCGGCTTCGGTGATGACGGGTGAACCTCTGACACATGACAGCTCCCGAGACGGTCA 60
DB 1 TCOCGGCTTCGGTGATGACGGGTGAACCTCTGACACATGACAGCTCCCGAGACGGTCA 60
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DB 61 CAGCTTGTCTGTAAGCGGATGCCGGAGCAGACAGCCCGTCAGGGCGCGTCAGCGGGTG 120
QY 121 TTGCGGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTTGACTCAGAGTGC 180
DB 121 TTGCGGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTTGACTCAGAGTGC 180
QY 181 ACCATATGAGCTTTTTCGCAAGCGCTAGGCGCTCCAAAGAGCTCTCTCACTACTTCTGG 240
DB 181 ACCATATGCGG-----TGTAATACCGCACA 207
QY 241 AATAGCTCAGAGCGGAGGGGCTCGGCCCTCTGCTAATAAATAAATAAATAGTCAGCCA 300
DB 208 GATGCGTAAGGAGAAATACCGCATCAG-----235
QY 301 TGGGGCGGAGAAATGGCGGAACTGGGCGGGAGGGAATATTGGCTATTGGCCATTGCCAT 360
DB 236 -----ATTGGCTATTGGCCATTGCCAT 256
QY 361 ACCTTGTATCTATATCATATATGATATTAATTTGGCTCATGTCCAAATATCAGCGCCA 420
DB 257 ACCTTGTATCCATATCATATATGATATTAATTTGGCTCATGTCCAAATATCAGCGCCA 316
QY 421 TGTGACATGATTAATGACTAGTTATTAATAGTAATCAATTAACGGGGTCAATTAATTCAT 480
DB 317 TGTGACATGATTAATGACTAGTTATTAATAGTAATCAATTAACGGGGTCAATTAATTCAT 376
QY 481 AGCCCATATATGAGTTCCGGTTACATTAATACGTAATTAATGCGCGCGCTGCTGACCG 540
DB 377 AGCCCATATATGAGTTCCGGTTACATTAATACGTAATTAATGCGCGCGCTGCTGACCG 436
QY 541 CCCAAGACCCCGCCCAATTGAGCTCAATTAATGAGCTATGTTCCCATAGTAAGCCCAATA 600
DB 437 CCCAAGACCCCGCCCAATTGAGCTCAATTAATGAGCTATGTTCCCATAGTAAGCCCAATA 496
QY 601 GGGACTTTCCATTGA CGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTTGGCAGTA 660
DB 497 GGGACTTTCCATTGAGCTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTTGGCAGTA 556
QY 661 CATCAAGTGTATCATATGCGAGTCCGCCCTTATTGAGCTCAATGACGGTAATGGCCC 720
DB 557 CATCAAGTGTATCATATGCGAGTACGCCCTTATTGAGCTCAATGACGGTAATGGCCC 616
QY 721 GCCTGGCATTAATGCCAGTACATGACCTTACGGGACTTTCTCTACTTTGGCAGTACATCTAC 780
DB 617 GCCTGGCATTAATGCCAGTACATGACCTTATGGGACTTTCTCTACTTTGGCAGTACATCTAC 676
QY 781 GTATTAGTCATCGCTATTACATGGTGTGCGGTTTGGCAGTACCAATGGCGGTGGA 840
DB |

DB 677 GTATTAGTCATCGCTATTACCATGTGTGATGCGGTTTTGGCAGTACATCAATGGCGGTGGA 736
QY 841 TAGCGGTTTTGACTACACGGGATTTCCAAAGTCTCCACCCATTCAGCTGCAATGGGAGTTTG 900
DB 737 TAGCGGTTTTGACTACACGGGATTTCCAAAGTCTCCACCCATTCAGCTGCAATGGGAGTTTG 796
QY 901 TTTTGGCACCAAAATCAACGGGACTTTCCAAATATGTCGTAATAACCCCGCTTTGACG 960
DB 797 TTTTGGCACCAAAATCAACGGGACTTTCCAAATATGTCGTAATAACCCCGCTTTGACG 856
QY 961 CAAATGGCGGTAGGGCTGTACGGTGGGAGTCTATATAAGCAGAGCTCGTTTTAGTGAAC 1020
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QY 1021 CGTCAGATCGCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAACACCCGGAC 1080
DB 917 CGTCAGATCGCTGGAGAGGCCATCCACGCTGTTTTGACCTCCATAGAACACCCGGAC 976
QY 1081 CGATCCAGCTTCGGCGCGGGAACGGTGCATTTGGAACCGGATTCCTCGTGCAGAGT 1140
DB 977 CGATCCAGCTTCGGCGCGGGAACGGTGCATTTGGAACCGGATTCCTCGTGCAGAGT 1036
QY 1141 GAGCTAAGTACCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGATGCTATA 1200
DB 1037 GAGCTAAGTACCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGATGCTATA 1096
QY 1201 CTGTTTTTGGCTTTGGGGCTTATACACCCCGC--TCCTTATGCTATAGGTGATGCTATAGC 1259
DB 1097 CTGTTTTTGGCTTTGGGGCTTATACACCCCGCTTCTTATGCTATAGGTGATGCTATAGC 1156
QY 1260 TTAGCCTATAGGTGTTGGTATTGACCAATTTAGCACCTCCCTCTTATGTTGACGATCT 1319
DB 1157 TTAGCCTATAGGTGTTGGTATTGACCAATTTAGCACCTCCCTCTTATGTTGACGATCT 1216
QY 1320 TTCCATTACTAATCAATACATGGCTTTTGCACAACTATCTCTATTTGGCTATATGCCA 1379
DB 1217 TTCCATTACTAATCAATACATGGCTTTTGCACAACTATCTCTATTTGGCTATATGCCA 1276
QY 1380 ATACTCTGCTTTCAGAGACTGACACGGACTCTGTATTTTACAGATGGGT--CAATTT 1438
DB 1277 ATACTCTGCTTTCAGAGACTGACACGGACTCTGTATTTTACAGATGGGTCCCATTT 1336
QY 1439 ATTATTACAAATTCATATACAAACCGCGTCCCGTCCCGTCCCGCAGTTTTTATATAA 1498
DB 1337 ATTATTACAAATTCATATACAAACCGCGTCCCGTCCCGCAGTTTTTATATAA 1396
QY 1499 CATAGGTGGGATCTCC---GACATCTCGGTACGTTTCCGGACATGGGCTCTCTCCG 1555
DB 1397 CATAGGTGGGATCTCCCGGAACTCTCGGGTACGTTTCCGGACATGGGCTCTCTCTCCG 1456
QY 1556 GTAGCGCGGAGCTTCCACATCCGAGCCCTGGTCCCATCCGTCACGCGCTCATGTCGC 1615
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DB 1577 CCACAGTGTGCGCACAAGGCGGTGGCGGTAGGGTATGTCTGTAATAGCTCGGAG 1636
QY 1736 ATTGGCTCGCAC--CTGGAGCGAGATGGAAGACTTAAGCAGCGGCGGAGAGATGTCAG 1794
DB 1637 ATTGGCTCGCACCGGCTGACAGATGGAAGACTTAAGCAGCGGCGGAGAGATGTCAG 1696
QY 1795 GCAGCTGAGTTGTGTATTCTGATTAAGACTCAGAGGTAACTCCCGTTGGGTGCTGTAA 1854
DB 1697 GCAGCTGAGTTGTGTATTCTGATTAAGACTCAGAGGTAACTCCCGTTGGGTGCTGTAA 1756
QY 1855 CGGTGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTCGCGCGCGCCACAGACATA 1914
DB 1757 CGGTGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTCGCGCGCGCCACAGACATA 1816

1915 ATAGCTGACAGACTAAACAGACTGTTCTTTTCCATGGGTCTTTTCTGAGTCAACCGTCGTC 1974
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1975 GACGAATTCAAGCAATCATGGATG-CAATGAGAGAGGCTCTGCTGTGCTGCTG 2033
1877 GACACGTGTGATCAGATATCGCGCGCTCTAGAGATATCGCGCATCGGCGCAGATCGT 1936
2034 TGTGGAGCAGTCTTCGTTCGCGCCAGCGCTAGCGAAACCCACG-TCACCGGGGGAAGTGC 2092
1937 GACCTTCTCCAGGAGTGCCCATGTGATCGAGGAGTGATGAAATCATGCTGTGATCGC 1996
2093 CGGCCACATGCTGTGCTGTGATTTGTTAGCTCTCTCGCACAGGCGCCGACAGAACGTCGA 2152
1997 CTTGAGCGTCTGCGCGCTGCTGAAGGCGCTGTACAACTTCGCCACCTGCGCGCTGTGGG 2056
2153 GCTGATCAACACCAACCGCAGTTGGCACCTCAATAGCAGCGCCCTGAACTGCAATGATAG 2212
2057 CTTGGTGACCTTCTCTGCTGTGCGGCAGGAGCTGCACACAGCCTGTACAAAGGCGGT 2116
2213 CTTCAACACCGCTGTGTGCGAGGCTTTTCTATCAACCAAGTTCAACTCTTTCAAGGCTG 2272
2117 GTACGAGCTGCAGACCTGAGCTGAACATGGAGACCTGAAATGACCATGCCCTGAG 2176
2273 TCCGTGAGAGCTAGCCAGCTGCGGACCCCTTACCGAATTTTGACAGGCTGGGCGCCCTAT 2332
2177 CTGCACCAAGAAACACAGCACCACTACATCATGTGTGGGCAACGACGCGGCTGTGAGCT 2236
2333 CAGTTATGCCAAGGAAGCGGCCCGCCAGCGCCCTACTGCTGCGCATACCCCCCAAA 2392
2237 AACCTTGACCAACACGAGCATCATCAACCAAGTTCTGCAACTGAGCGACGCCACAA 2296
2393 ACCTTGCGGTATTGTGCGCGC---GAAGAGTGTGTGTGTGTCGGTATATTGCTTTCACTCC 2449
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2450 CAGCCCCGTGTGTGGAGCAAGCAAGGTCGGGCGGCCCACTCAAGCTGTGGGTGA 2509
2357 CAACTTCAACCACTAGCGGCCATGAGCTGCGACTTCAACGGCGGCAAGATCAGCGTGCA 2416
2510 AAATGATAGGAGCTTCTGCTCTTAAATACAGCGCCACCGCTGGGCAATTGTTTCGG 2569
2417 GTACAACTGTAGCCACAGCTACGCCGGCGACGCCGCCAACCACTGCGGCACCGTGCCAA 2476
2570 TTGTACTGTGATGAATCAACTGGAATTCACAAAGTGTGGGAGCGCCCTTGTGTGAT 2629
2477 CGGCGTGTGCAGACCTTCTATGAGGATGGCTTGGGCGGCAGCTACATCGCCCTGGACAG 2536
2630 CGGAGGGCGGGCAACAAACCTGCACTGCCCCACTGATGTTGTTCCGCAAGCATCCGGA 2689
2537 CGGCAAGGGCAACTGGGACTGCAATCATGACCACTACAGTACCTGATCATCCAGAACAC 2596
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2597 CACTTGGAGGACACTGCGCAGTTACGAGGCGCCAGCCCATCGGTACTTGGGCGCTGCT 2656
2750 CCGTATAGGCTTTGGCATATTCTTGTACCATCAACTACCATATTTAAATACAGGAT 2809
2657 GAGCCAGAGGACCAAGGACATCTACATACGAGAGGCTGCTGGGCACCTTCACTCTGAC 2716
2810 GTACGTGGAGGGGTGCAACACAGGCTGGAGTGTGCTGCAACTGGAACGCGGGGCGAAG 2869
2717 CTTGAGCGACAGCGAGGGCAAGGACACACCGCGCGCTACTGCTGACAGGTGTGCT 2776
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2930 CTTAGGACCCCTGCTGTGTTACAGCGGGGTTTTTTCTTGTGTAAGAAATCTCTCAAT 2989
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2990 ACCGACAGTCTAGACTCGTGTGGACTTCTCTCAATTTTCTAG-GGGGATCTCCCGTGT 3048
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3049 GTCTTTGGCCAAAATTCGCGAGTCCCAACCTCAATCAGCTCACCAACCTCTGTCTCTCAA 3108
2957 CAACGACGAGTGATCATGAAGAACCACTGAGGACATCATGGGCATCCCTACTACTGCAA 3016
3109 TTTGTCTCTGGTTATCGCTGAGATGTGTCTGCGC-----GTTTTATCATATTCTCTTCAT 3163
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3164 CTTGCTGTCTATGCTCATCTTCTTATTG-GTTCTTCTGATTTATCAAGTATGTTGCCCG 3222
3077 CTGGCTGTGAGCAACGCGCAGCTACTGAAACGAGACCCACTTCAGCGACGACATCGAGCA 3136
3223 TTTGTCTCTTAATTCAGGATCAACAAACACAGTACGGGACATGCACAAAACCTGCACGA 3282
3137 GCAGGCGGACATGATCACCAGATGCTGCAGAAAGGAGTACATGGAGGAGGCGCAA 3196
3283 CTCCTGCTCAAGGCAACTCTATGTTTC---CTCATGTTGTGTATACAAACCTACGGATG 3339
3197 GACCTGAAACAGCTGGATCCAGATCTGCTGTGCTTCTAGTTGCCAGCCATCTGTTGTTT 3256
3340 GAAATTGCACCTGTATTCCCATCCCATCGTCTGGGCTTTTCGCAAAATACCTATGGAGT 3399
3257 GCCCTTCCCGCTGCTTCCCTTGAGCCCTGGAAGGTGCCACTCCCACTGTCTTCTCTAAT 3316
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3460 GGGCTTCCCGCTGTTTGGCTTTTCACTATATGAGTATGAGTATGTTGGGGCCAAAGTC 3519
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3520 TGTAAGATCTGTGAGTCCCTTTATACCGCTTATACCAATTTTCTTTCTCTCTGGGTAT 3579
3437 TGGGCTCTATGGGTACCCAGGTGCTGAAGAAATTGACCCCGGTTCTCTCTGGGCCAAGAA 3496
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3497 AGCAGGCATCCCTCTTC-TGTGACACACCTGTCCAGCGCCCTGGTCTTAGTTCCA 3555
3640 CTACGCGTTAGAGTCTGCTGATCAGCTCGACTGTGCTTCTAGTTGCGAGGCATCTGTT 3699
3556 GCCCACTCATAGGACACTCATAGCTCAGGAGGGCTCCGCTTCAATCCACCCGCTAAA 3615
3700 GTTTGCCCCCTCCCGTCTCTTGACC-----CTGGAAGGTGCCCACTCCCACTGTC 3753
3616 GTACTTGGAGCGGTCTCTCCCTCCCTCATAGCCCAACCAACCTAGCCCTCCAAG 3675
3754 CTTTCTTAATAAAATGAGGAAATTCATCGCATTTGCTGAGTAGTGTCTATTCTTCTG 3813
3676 GTGGGAGAAATTAAGCAAGATAGGCTATTAGTGCAGAGGGAGAGAAATGCGCTCAA 3735
3814 GGGGTGGGGTGGGCGAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGGCATGCT 3873
3736 CATGTGAGGAAGTAATGAGAGAAATCATAGAAATTTTAAGGCCATGATTTAAGGCCATCAT 3795
3874 GG-GGAGCTTTCCGCTCTCGCTCAGTCACTCGCTGCGCTCGGTCGTTTCGGCTCGGCG 3932
3796 GGGCTTAATCTTCCGCTTCTCGCTCAGTCACTGCTGCTGCGTCTGGTCTGGCTCGGCG 3855
3933 GAGCGGTATCAGTCACTCAAAAGGGGTAATACGGTTATCCACAGAAATCAGGGGATAACG 3992
3856 GAGCGGTATCAGTCACTCAAAAGGGGTAATACGGTTATCCACAGAAATCAGGGGATAACG 3915
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3916 CAGGAAGAAATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCCGCT 3975
4053 TGCTGCGGTTTTTTCATAGGCTCCGCCCTTCGAGCATCACAAAAATCGACGCTCAA 4112

Db 2102 CCCTTTGGCTCTATGTCATGCTATACGTGTTTTTGGCTTGGGGCTATACACCCCGCTCC 2161
QY 1236 TTATGCTATAGGTGATGGTATAGCTTAGCTATAGGTGTTGGTTATATGACCAATTTATGAC 1295
Db 2162 TTATGCTATAGGTGATGGTATAGCTTAGCTATAGGTGTTGGTTATATGACCAATTTATGAC 2221
QY 1296 CACTCCCTTATTGGTGACCATATCTTCCATTAATTAATCAATCAATGAGTCTTTTGGCCACA 1355
Db 2222 CACTCCCTTATTGGTGACCATATCTTCCATTAATTAATCAATCAATGAGTCTTTTGGCCACA 2281
QY 1356 ACTATCTCTATTGGCTATATGCAATACCTCTGTCTTTCAGAGACTGACACGGACTCTGTGA 1415
Db 2282 ACTATCTCTATTGGCTATATGCAATACCTCTGTCTTTCAGAGACTGACACGGACTCTGTGA 2341
QY 1416 TTTTTCACAGGATGGGGT - CCA TTTTATTTTAAATTCACATATACAAACAACGGCGTCC 1474
Db 2342 TTTTTCACAGGATGGGGTCCCA TTTTATTTTAAATTCACATATACAAACAACGGCGTCC 2401
QY 1475 CCGGTGCCCGCAGTTTATTAATAACATAGGTGGGATCTCC - - GACATCTCGGGTACGT 1531
Db 2402 CCGGTGCCCGCAGTTTATTAATAACATAGGTGGGATCTCCACGGCAATCTCGGGTACGT 2461
QY 1532 GTTCCGGACATGGGCTCTTCTCCGGTAGCGGGAGCTTCCACATCCGAGCCCTGGTCC 1591
Db 2462 GTTCCGGACATGGGCTCTTCTCCGGTAGCGGGAGCTTCCACATCCGAGCCCTGGTCC 2521
QY 1592 ATCGGTCCAGGGCTCATGGTCTCGGAGCTCTTGTCTCTTAACAGTGGAGGCGAGAC 1651
Db 2522 ATCGCTCCAGCGCTCATGGTCTCGGAGCTCTTGTCTCTTAACAGTGGAGGCGAGAC 2581
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Db 2582 TTAGGCACAGCACAAATGCCACACACAGTGTGCCGACAGGCGGTGGCGGTAGGGT 2641
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Db 2642 ATGTGTCTGAAATGAGCTCGGAGATTGGGCTCGACCTCGACGCGCAGATGGAGACTTAA 2701
QY 1772 GGCAGCGCAGAGAAAGATGCGAGGAGCTGAGTTGTTGTTATCTGATTAAGAGTCAAGGT 1831
Db 2702 GGCAGCGCAGAGAAAGATGCGAGGAGCTGAGTTGTTGTTATCTGATTAAGAGTCAAGGT 2761
QY 1832 AACTCCGTTGGGTGCTGCTTAACGTTGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGC 1891
Db 2762 AACTCCGTTGGGTGCTGCTTAACGTTGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGC 2821
QY 1892 TGCAGCGCGCGCCACAGACATAAATAGCTGACAGACTAAACAGACTGTTCTTCCATGGG 1951
Db 2822 TGCAGCGCGCGCCACAGACATAAATAGCTGACAGACTAAACAGACTGTTCTTCCATGGG 2881
QY 1952 TCTTTTCTGAGTCAACGTCGTGCGAATTCAGCAATTCATGGATGCAATGAAGAGAGG 2011
Db 2882 TCTTTTCTGAGTCAACGTCGTGCGAATTCAGCAATTCATGGATGCAATGAAGAGAGG 2097
QY 2012 GCTCTGCTGTGTGCTGCTGTGTGGAGCTCT - - - TCGTTTCCCGCAGCGCTAGCGA 2068
Db 2938 ACTTCCCTAAGAGCTACTACATAACAAGAAAATGGCAACTATGGAAGAAAATCCAGAGA 2997
QY 2069 AACCCACGTCACCGGGGGAAGTGCCGGCCACACTGTGTCTGGATTGTTAGGCTCTCTCGC 2128
Db 2998 GAAATCAGTGTCTACAGAGGGGAGCTTGTGATAGCAGCGCAGAGGTCAAGGATGCAGAA 3057
QY 2129 ACAGGGCCAGAGAGAAAGTCAAGCTGATCAACACCAACCGGAGTTGGCACTCTCAATAG 2188
Db 3058 AAGCAGTATGAGAAAGATCCTGATGACTTAAACAGAGGGCACTGCATGATCGGAGAGT 3117
QY 2189 CAGCGCCCTGAATGCAATGATAGCTCTCAACCGGCTGTTGGCAGGGCTTTCTATCA 2248
Db 3118 GTCCGAGCTTCAATACAAATCAAAAATGATGAATTAAGGGCCAACTTCCGACAGATTG 3177
QY 2249 CCACAGTTCAACTCTTTCAGGCTGTCTTCCAGAGGCTTAGCAGGTGCGGACCCCTTACCGA 2308
Db 3178 CAGCAGGGAAGAACATCCCGGGCAGGACCGGGATCTCTACAGGGGTAGAGCCAGGTGATCAT 3237

QY 2309 TTTTGACAGGCGCTGGGGCCCTATCAGTTATGCCAAACGGAAGCGGCCCGGAC - - - CAGC 2364
Db 3238 CTTAAGGAAGATACGCACTAAGCTACGGGAATACACTGGACCTGAATAGTCTTGACATT 3297
QY 2365 GCCCTACTCTGCTGGCACTACCCCCCAAAACCTTGGCGGTATTTGTCGCCGGAAGAGTGTGT 2424
Db 3298 GATGAACCTACAGGACAGACAGCTGATTTGGCTGACCAATAATTTGTCTATCTGACATCTTC 3357
QY 2425 GTGGTCCGG - - - - - TATATTGCTTCACTCCAGCCCCCTGTGTGGTGGGA 2468
Db 3358 GTGGTCCCGATCATCTTGAAAGCACTGTACATGTTTAAACAAACGAGGTAGGCAGACTTCA 3417
QY 2469 AGCAGCGACAGTCTGGGGCGGCCCACTACAGTGGGGTGAATAATGATACGACGCTCTTC 2528
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QY 2529 GTCTTTAACAATPACAGGCCACCGCTGGGCAATTTGGTTGTATACCTTGGATGAATCA 2588
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Db 3538 GCTGAAGAGATAAACACAGGAAGATTCCGCACTGCAGTATGTGGACTATATCTTCACACAG 3597
QY 2649 ACCCTGCACTGCCCACTGATTGCTTCCGACAGCATCCGAGCGCCACATCTCTCGGTGC 2708
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QY 2769 TATCCTTGTACC - - - - - ATCAACTTACACCATATTTTAAATCAGGATGTA 2812
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QY 2813 CGTGGAGGGGTGCAACACAGGCTGGAACTGCTTCCCACTGGAGCGGGCGGAAGTTG 2872
Db 3778 CAAGTGCATCTTGCAGGGATGGAGCCAAAGGAATTTCAAGCCCTCAGGCAACATTCAAAG 3837
QY 2873 CGATCTGGAAGATAGGGACAGGTCCGAGATCGATATGGAGAAACATACATCAGGATTCCT 2932
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QY 2933 AGGACCCCTGCTGCTGTGTACAGGCGGGTGTCTTGTGTGAACAAG - - - - - 2978
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QY 2979 - - - - - ATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTCTAGGG 3035
Db 3958 GCTTCTTCTTATATCTTCAAGATATGAGGAACAATCATGCTTCAAAAATCTGTGGGC 4017
QY 3036 GATCTCCCGTGTGTCTTGGCCAAAATTCGAGTCCCAACCTCCAATCACTCAC - - - - - 3090
Db 4018 ACAGCTGATGAAGAGCTTCCGAAGAAATCATCATTTCTATCAATCATCTCAGACGCA 4077
QY 3091 CAACTCCTGCTCCTCAATTTGTCTGTGTTATCGTGTGAATGTCTGCGGCGTTTATCA 3150
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QY 3151 TATTCTCTTCTCATCTGCTGCTATGCCCTCATCTTCTTATTTGGTCTTCTGGATTATCAAG 3210
Db 4138 AAGGAGGAGTGGACAACATTTTCATCTCGGTGATGATGGAATCCAGAGCTTCGTAGCCTG 4197
QY 3211 GTATGTTGCCGCTTGTCTCTTAAATTCAGGATCAACAAACACAGTACGGGACCATGCA 3270
Db 4198 GCTCAGATCTTGATTTGACCAAGAAATCTCAAAACAGGAACTTATGAATTA 4257
QY 3271 AAACCTGCACGACTCCTGCTCAAGGCACTCATGTTTCCCTCATGTTCTGCTGTACAAAC 3330
Db 4258 TAAGTACATAATATAATCAATCACTACTATAGTTTAAAGAAATACTAATCATTTAGTTA 4317

Query Match		40.8%;	Score 2397.8;	DB 17;	Length 6050;
Best Local Similarity		72.1%;	Pred. No. 0;		
Matches 3456;		Conservative	0;	Mismatches 1097;	Indels 240; Gaps 16;
QY	337	ATTATTGGCTATTGGCCATTGTCATAGTGTGTATCTATATCATATAATATGACATTATATTT	396		
DB	1263	AATATTGGCTATTGGCCATTGTCATAGTGTGTATCTATATCATATAATATGACATTATATTT	1322		
QY	397	GGCTCATGTCCAATATGACCGCCATGTGACATTTGACATTTATGACTAGTTATTAATAGTAA	456		
DB	1323	GGCTCATGTCCAATATGACCGCCATGTGACATTTGACATTTATGACTAGTTATTAATAGTAA	1382		
QY	457	TCAAATTACGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGCTTACATAACTTACG	516		
DB	1383	TCAAATTACGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGCTTACATAACTTACG	1442		
QY	517	GTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCATATAATGACG	576		
DB	1443	GTAAATGGCCCGCTCG-TGACCGCCCAACGACCCCGCCCATTTGACGTCATATAATGACG	1501		
QY	577	TATGTTCCCATAGTAAAGCCCAATAGGACTTTTCCATTGACGTCAATGGGTGGAGTATTTA	636		
DB	1502	TATGTTCCCATAGTAAAGCCCAATAGGACTTTTCCATTGACGTCAATGGGTGGAGTATTTA	1561		
QY	637	CGGTAACTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTAT	695		
DB	1562	CGGTAACTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGGCCCCCTAT	1621		
QY	696	TGACGTCAATGACGTAATATGGCCCGCTGGCATTTATGCCAGTACATGACCTTTACGGGA	755		
DB	1622	TGACGTCAATGACGTAATATGGCCCGCTGGCATTTATGCCAGTACATGACCTTTACGGGA	1681		
QY	756	CTTTCCTACTTGGCAGTACATCTACGTATTTAGTTCATCGCTATTACCATGGTGTATGCGTT	815		
DB	1682	CTTTCCTACTTGGCAGTACATCTACGTATTTAGTTCATCGCTATTACCATGGTGTATGCGTT	1741		
QY	816	TTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTACCGGGATTTCCAGTCTCCA	875		
DB	1742	TTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTACCGGGATTTCCAGTCTCCA	1801		
QY	876	CCCAATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATG	935		
DB	1802	CCCAATTGACGTCAATGGGAGTTTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATG	1861		
QY	936	TCGTATAACCCCGCCGTTGACGAAATGGCGGTAGCGGTGTACGTTGGAGGTCTA	995		
DB	1862	TCGTATAACCCCGCCGTTGACGAAATGGCGGTAGCGGTGTACGTTGGAGGTCTA	1921		
QY	996	TATAACGAGCTCGTTTATGTGAACCGTCAAGTCGCTGGAGACGCATCCACGCTGTTT	1055		
DB	1922	TATAACGAGCTCGTTTATGTGAACCGTCAAGTCGCTGGAGACGCATCCACGCTGTTT	1981		
QY	1056	TGACCTCCATAGAAGACACCGGACCGGATCCAGCCTCCGCGGCCGGAAACGGTGCATTGG	1115		
DB	1982	TGACCTCCATAGAAGACACCGGACCGGATCCAGCCTCCGCGGCCGGAAACGGTGCATTGG	2041		
QY	1116	AACCGGATTTCCCGTCCCAAGAGTGAAGTGAAGTACCGCCTATAGACTCTATAGGCACAC	1175		
DB	2042	AACCGGATTTCCCGTCCCAAGAGTGAAGTGAAGTACCGCCTATAGACTCTATAGGCACAC	2101		
QY	1176	CCCTTTGGCTCTTATGCATGCTACTCTGTTTGGCTTGGGGCTATACACCCCGCTCC	1235		
DB	2102	CCCTTTGGCTCTTATGCATGCTACTCTGTTTGGCTTGGGGCTATACACCCCGCTCC	2161		
QY	1236	TTATGCTATAGGTGATGGTATAGCTTATAGCTATAGGTGTGGGTATTTGACATTATTGAC	1295		
DB	2162	TTATGCTATAGGTGATGGTATAGCTTATAGCTTATAGGTGTGGGTATTTGACATTATTGAC	2221		
QY	1296	CATCCCTCTATTGGTGACGATATTTCCATTAATAATCCATAAATGAGTGTCTTTGGCACA	1355		
DB	2222	CATCCCTCTATTGGTGACGATATTTCCATTAATAATCCATAAATGAGTGTCTTTGGCACA	2281		
QY	1356	ACTATCTCTATTGGCTATATGCCAATACTCTGTCTCTCAGAGACTGACACGGACTCTGTA	1415		
DB	2282	ACTATCTCTATTGGCTATATGCCAATACTCTGTCTCTCAGAGACTGACACGGACTCTGTA	2341		
QY	1416	TTTTTACAGATGGGT-CCATTATTTATTTACAAATTCACATATCAACAACCGCTCC	1474		
DB	2342	TTTTTACAGATGGGTCCCATTTATTTACAAATTCACATATCAACAACCGCTCC	2401		
QY	1475	CCGTCGCCCGAGTTTTTTTATTTAAACATAGCTGGGATCTCC---GACATCTCGGTAAGT	1531		
DB	2402	CCGTCGCCCGAGTTTTTTTATTTAAACATAGCTGGGATCTCCACGCGAATCTCGGTAAGT	2461		
QY	1532	GTTCGGACATCGGCTCTTCTCGGTAGCGGGAGCTTCCACATCCGAGCCCTGTGTCC	1591		
DB	2462	GTTCGGACATCGGCTCTTCTCGGTAGCGGGAGCTTCCACATCCGAGCCCTGTGTCC	2521		
QY	1592	ATCCGTCCAGCGCTCATGTCGCTCGGAGCTCTTGTCTCTTAAACAGTGGAGCCAGAC	1651		
DB	2522	ATCCGTCCAGCGCTCATGTCGCTCGGAGCTCTTGTCTCTTAAACAGTGGAGCCAGAC	2581		
QY	1652	TTAGGCACAGCAATGCCCAACCAACAGTGTGCCGCAACAGCCGTGGCGGTAGGTT	1711		
DB	2582	TTAGGCACAGCAATGCCCAACCAACAGTGTGCCGCAACAGCCGTGGCGGTAGGTT	2641		
QY	1712	ATGTGTCGAAATGAGCTCGGAGATTGGCTCGCACCTGGACGAGATGGAAGACTTAA	1771		
DB	2642	ATGTGTCGAAATGAGCTCGGAGATTGGCTCGCACCTGGACGAGATGGAAGACTTAA	2701		
QY	1772	GGCAGCGGACAGAGATGCGGAGCTGAGTTGTTGTTATTTCTGATAAGAGTCAAGGT	1831		
DB	2702	GGCAGCGGACAGAGATGCGGAGCTGAGTTGTTGTTATTTCTGATAAGAGTCAAGGT	2761		
QY	1832	AATCCCGTTGGCTGCTGTTAAACGTTGAGGGCAGTGTAGTCTGACGAGTACTCTGTC	1891		
DB	2762	AATCCCGTTGGCTGCTGTTAAACGTTGAGGGCAGTGTAGTCTGACGAGTACTCTGTC	2821		
QY	1892	TGCGCGCGCGCCACAGACATAATAGCTGACAGACTTAAACAGACTGTTCTCTTCCATGGG	1951		
DB	2822	TGCGCGCGCGCCACAGACATAATAGCTGACAGACTTAAACAGACTGTTCTCTTCCATGGG	2881		
QY	1952	TCCTTTCTCAGTACCCGTGTCGACGAATCAAGCAATCATGGATGCAATGAAGAGAGG	2011		
DB	2882	TCCTTTCTCAGTACCCGTGTCGACGAATCAAGCAATCATGGATGCAATGAAGAGAGG	2937		
QY	2012	GCTCTGCTGTGCTGCTGCTGTGGAGCAGTCT---TCGTTTCCCGCCAGCGCTAGCGA	2068		
DB	2938	ACTCCCTTAAAGAGCTACTACACTAACAGAAAAATGGCAACTATGGAAGAAATCCAGAGA	2997		
QY	2069	AACCCACGTCACCGGGGAAAGTCCCGCCACACTGTGTCTGGATTGTTAGCCTCTCTCGC	2128		
DB	2998	GAATCAGTGTCTACGAGGGGACGTTGTGATAGCAGCCAGCAAGGTCAAGGATGCAGAA	3057		
QY	2129	ACCAGCGCCAAAGCAGAACGTCAGCTGATCAACCAACAGCGAGTTGGCACTCAATAG	2188		
DB	3058	AAGCAGTATGAGAAAGGATCTGTATGACTTTAAACAGAGGGCAGCTGATGATCGGAGAGT	3117		
QY	2189	CAGGCGCTTGAATGCAATGATAGCCTCAACCCGCTGGTGGCAGGGCTTTCTATCA	2248		
DB	3118	GTGCGAGCTTCAATACAATCAAAAAATTGATGAATGAAGCGCCAACTTGCCCGACAGATTG	3177		
QY	2249	CAACAAGTTCAACTCTTCAGGCTGCTCTGAGAGGCTAGCCAGCTGCCACCCCTTACCGA	2308		
DB	3178	CAGCAGGGAAGAACATCCGGGCAGACCCGGATCTTACAGGGGTAGAGCCAGGTGATCAT	3237		
QY	2309	TTTTGACAGGGCTGGGGCCCTATCAGTTATGCAACGGAAGCGGCCCGAC----CAGC	2364		
DB	3238	CTTAAGGAAGATCAGCACTAAGCTACGGGAATACACTGGACCTGAATAGTCTTGACATT	3297		
QY	2365	GCCCTACTCTGGCACTACCCCAAAACCTTGGGTATGTCGCGGAGAGTGTGT	2424		
DB	3298	GATGAACCTACAGGACAGACAGCTGATTGGCTGACCAATTAATGTCATCTGACATCATTC	3357		
QY	2425	GTGGTCCGG-----TATATTGCTTCACTCCACGCCCCGTGGTGGGA	2468		

Db 3358 GTGGTCCCGATCATCTTTGAAGGCATGTATACATGTTAAACAACAGAGGTAGGCGACTTCA 3417
Qy 2469 ACACCCACAGAGTTCGGCGCGCCACCTACAGCTGGGGTGAATAATGATACGGAGCTCTTC 2528
Db 3418 AAGGACAACAAGGGATGAGATCAGATTCAGAGTACAGCTCATATAGGATGTCAAT 3477
Qy 2529 GTCCCTTAACAATACCAAGCCACCGCTGGGCAATGGTTCGGTTGTACCTGGATGAATCA 2588
Db 3478 GGAATCAGAAAGCCCAACAATCTGTATGTCAATGCCAAAGCCCAATCCAGCATGAAG 3537
Qy 2589 ACTGGATTACCAAGATGTGGGAGCGCTCTTGTGTATCATCGAGGGGGCGGCAACAC 2648
Db 3538 GCTGAAGAGATAACAACAGGAATCTCCGCACTGCAATGTGGAATATATCTGACACAG 3597
Qy 2649 ACCCTGCATCGCCCACTGATTGCTTCGCAAGCATCCGACGCCACATCTCTCGGTGC 2708
Db 3598 ATAAAGCAGGAATATGTTAAGCCCTGTCTAGTGTAGTTGGTCTTGGCACTGGCA 3657
Qy 2709 GGCTCCGGTCCCTGGATCACACCCAGGTGCTCGTGCAGTACCCGTATAGGCTTTGGCAT 2768
Db 3658 AAAGACTGGACATCGAGAAATTTGAAGATGCTCGGTGCACCCCTGCAAAATTCATGGCGGAG 3717
Qy 2769 TATCTTTGACC-----ATCAACTACACATATTTAAATCAGGATGA 2812
Db 3718 TCTCTTATTGCGGGAGTTTATCTGGGAATCTGTGAATCGTGAATATATCAGACAGAG 3777
Qy 2813 CGTGGGAGGGTCAACACAGGCTGGAAGCTGCTGCAACTGACCGGGCGCAAGCTTG 2872
Db 3778 CAAGGTGCATTCGAGGATGGAGCCAAAGGAATTTCAAGCCCTCAGGCAACATTTCAAAG 3837
Qy 2873 CGATCTGGAGATAGGACAGGTCGAGATCGATATGGAGAACATCACATCAGGATTTCCCT 2932
Db 3838 GATGCTGGATGTACATAGTTGAACATATTTAGTTCACCATCATCAATATGCGGTGTTTGTCT 3897
Qy 2933 AGAACCCCTGCTGCTGTTACAGGGGGGTTTTCTTGTGTGCAAGA----- 2978
Db 3898 GGGGCCCCCTGATAGGTGTCCACCAACATGCTGTTGTCGAGGGATGGCTGAATTAGGT 3957
Qy 2979 ---ATCTCACATACCGAGAGTCTAGACTCGTGTGGAGTCTCTCAATTTTCTAGGG 3035
Db 3958 GCCTTCTTTTATCTTCAGGATATGAGGAACACATCATGCTTCAAAAACCTGTGGGC 4017
Qy 3036 GGATCTCCCGTGTCTTGGCCAAAATTCGAGTCCCACTCCCAATCACTCAC----- 3090
Db 4018 ACAGCTGATGAAAAGCTTGGAAAGAAATCATCATCTCAATCATACCTCAGACGCACA 4077
Qy 3091 CAACCTCTGCTCTCAATTTGCTGGTTATCGCTGGATGTGTCTGGCGGTTTTATCA 3150
Db 4078 CAATCAATGGGAATACAACTGGACCAAGAGGATAATTTATGTTATGTTGCTGGCGGA 4137
Qy 3151 TATTCTCTTCATCTGCTATGCTCATCTTCTTATTTGTTCTCTGGATTATCAAG 3210
Db 4138 AAGGAGCAGTGGACAACCTTTCATCTCGGTGATGACATGGATCCAGAGCTTCGTAGCCTG 4197
Qy 3211 GTATGTTGGCCGTTGTCTCTAAATTCAGGATCAACAACAGCAGTACGGGACCATGCA 3270
Db 4198 GCTCAGATCTTGATGACCAAGTGAAGGAATCTCAACAGGAACTATGAATTA 4257
Qy 3271 AAACCTGCAGACTCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGCTGTACAAAAC 3330
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Qy 3331 CTACGGATGGAATTCGACCTGATTTCCCATCCCATCGTCTGGGCTTTCCGAAATATACC 3390
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Qy 3391 TATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTTTACTAGTGCCATTTGTTTCACT 3450
Db 4378 AGTTAAGTTAGCTAAATTTGATTTATATGATTTGTCACAATTAATGTAATCATAGACCAAT 4437
Qy 3451 GGTTCGTAGGGCTTTCCCCACCTGTTTGGCTTTTTCAGCTATATGAGTGA---TGTGGTAT 3507
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Qy 3508 GGGGCAAGTCTGTACAGCATCGTGCAGTCCCTTTTATACCGCTGT----- 3552
Db 4498 AGGGCAGGTCACTTAAAGTGACCTTTTGTATATATGATGTAGATTTCAATTGATC 4557
Qy 3553 -----TACCAATTTTCTTTTGTCTCTGGGATATACATTTAAGAAATTCAGACTCGAGC 3603
Db 4558 GAATACTAATCTCTGCTCTCTTTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4617
Qy 3604 AAGTCTAGAA-----AGCGCGCAAGATATACAGGATCCCACTACGCGTTAGAGC 3653
Db 4618 TCGTCCGAATTTGGCGCGGATCTCGCAATCCCTAGAGGATTAGGCAAGGGCTTGAGC 4677
Qy 3654 TGGC----- 3657
Db 4678 TCACGCTCTTGTGAGGGAAGAAATACAAATCAGGGGAGTATATGAATCTCCATCGAGA 4737
Qy 3658 -----TGATCAGCTTCGATCTGTGCTCTTAGTTGCCAGCATCTGTGTGT 3701
Db 4738 AACCCAGATCTACGTATGATCAGCTCGACTGTGCTCTTAGTTGCCAGCATCTGTGTGT 4797
Qy 3702 TTGCCCTCCCGCTGCTCTTGTGACCTGGAGGTGCACCTCCCACTGTCTCTTCTCTA 3761
Db 4798 TTGCCCTCCCGCTGCTCTTGTGACCTGGAGGTGCACCTCCCACTGTCTCTTCTCTA 4857
Qy 3762 ATAAATGAGGAATTTGCATCTGCTGAGTAGTGTCTATTTCTTCTGGGGGTGG 3821
Db 4858 ATAAATGAGGAATTTGCATCTGCTGAGTAGTGTCTATTTCTTCTGGGGGTGG 4917
Qy 3822 GGTGGGCGAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGGATCTCTGGGAGCT 3881
Db 4918 GGTGGGCGAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGGATCTCTGGGATGC 4977
Qy 3882 CTT----- 3884
Db 4978 GGTGGGCTCTATGGCTTTGAGCGGAAAGAACAGCTGGGGTCTCAGACTCGACTCTA 5037
Qy 3885 ---CCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3941
Db 5038 GAATTTCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 5097
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Qy 4062 TTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT 4121
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Qy 4122 GCGGAAACCCGACAGGACTATAAAGATACAGCGTTTCCCTGGAAGCTCCCTCGTGC 4181
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Qy 4302 CCAAGCTGGGCTGTGTGACGAAACCCCGTTTACGCCCCGCTCGCTCGCTTATTCGGTA 4361
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Qy 4362 ACTATGCTTGTAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGGAGGAGCCACTG 4421
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QY 4422 GTAACAGGATTACAGAGCGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGC 4481
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DB |||||||
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DB |||||||
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QY 5818 TGNCTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGATTTTGG 5877
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QY 5878 TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTAA 5937
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QY 4782 AATCAATCTAAAGTATATAGTAAGTAACTTGGTCTGACAGATTACCAATGCTTAATCAGTG 4841
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QY 5938 AATCAATCTAAAGTATATAGTAAGTAACTTGGTCTGACAGATTACCAATGCTTAATCAGTG 5997
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QY 4842 AGGCACCTATCTCAGCGGATCTGTCTATTTCGTTTCATCCATAGTTGCTGACTC 4894
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RESULT 5

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US-10-491-121-24
; Sequence 24, Application US/10491121
; Publication No. US20040259825A1
; GENERAL INFORMATION:
; APPLICANT: NABEL, GARY
; APPLICANT: YANG, ZHI-YONG
; APPLICANT: SULLIVAN, NANCY
; APPLICANT: SANCHEZ, ANTHONY
; TITLE OF INVENTION: Development of a Preventive Vaccine for
; TITLE OF INVENTION: Filovirus Infection in Primates
; FILE REFERENCE: NIH221.001NP
; CURRENT FILING DATE: 2004-03-26
; PRIOR FILING DATE: 2002-09-24
; PRIOR FILING DATE: 2002-09-24
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 6148
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct pVR1012-VP35
US-10-491-121-24
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Query Match 40.7%; Score 2395.6; DB 18; Length 6148;
Best Local Similarity 71.6%; Pred. No. 0;
Matches 3516; Conservative 0; Mismatches 1194; Indels 204; Gaps 20;
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QY 1 TCGCGGTTTCGGTGATGCGGTGAAACCTCTGACACATGACGCTCCCGAGACGGTCA 60
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QY 181 ACCATATGAAGCTTTTGTGCAAAAGCCTAGGCCTCCAAAAAGCCTCCTCACTACTTCTGG 240
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QY 181 ACCATATGCGG-----TGTGAATAACCGCACA 207
DB |||||||
QY 241 AATAGCTCAGAGCGCGAGCGCGCTCGGCCTCTGCATAAATAAAAAAATTAGTCAGCCA 300
DB |||||||
QY 208 GATGCGTAAGGAGAAAAATACCGCATCAG----- 235
DB |||||||
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QY 236 -----ATTGGCTTAATTGGCCATTTGCAT 256
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QY 257 AGCTTGTATCCATATCATATATATGTACATTTATATTGGCTCATGTCCAATATGACCGCCA 316
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DB |||||||
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DB |||||||
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DB |||||||
QY 1201 CTGTTTTTGGCTTGGGGCTATACACCCCGC-TCTTATGCTATAGGTGATGCTATAGC 1259
DB |||||||
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1097 Db |||||CTGTTTGGCTTGGGCTTATACACCCCGCTTCTTATGCTATAGGTGATGGTATAGC 1156
1260 QY TTAGCCTATAGGTGGTGTATTGACCATTTATGACCACTCCCTTATTTGGTGGAGTACT 1319
1157 Db TTAGCCTATAGGTGGTGTATTGACCATTTATGACCACTCCCTTATTTGGTGGAGTACT 1216
1320 QY TTCCATTACTAAATCCATAAATGCTCTTTGCCACAATCTCTATTTGGCTATATGCCA 1379
1217 Db TTCCATTACTAAATCCATAAATGCTCTTTGCCACAATCTCTATTTGGCTATATGCCA 1276
1380 QY ATACTCTGCTCTCAGAGACTGACCGGCTCTGTATTTTACAGATGGGT-CAATTT 1438
1277 Db ATACTCTGCTCTCAGAGACTGACCGGCTCTGTATTTTACAGATGGGTCCCAATTT 1336
1439 QY ATTATTTACAAATTCATATACAAACCGCTCCCGGTCCCGCAGTTTTTATTAA 1498
1337 Db ATTATTTACAAATTCATATACAAACCGCTCCCGGTCCCGCAGTTTTTATTAA 1396
1499 QY CATAGCGTGGATCTCC--GACATCTCGGTACGTGTTCCGGACATGGCTCTCTCCG 1555
1397 Db CATAGCGTGGATCTCCACGCGAATCTCGGTACGTGTTCCGGACATGGCTCTCTCCG 1456
1556 QY GTAGCGCGGAGTTTCCACATCCGAGCTGTGTCCTCATCCGTCAGCGGCTCATGTGCG 1615
1457 Db GTAGCGCGGAGTTTCCACATCCGAGCTGTGTCCTCATCCGTCAGCGGCTCATGTGCG 1516
1616 QY TCGGAGCTCTTGTCTTAAACAGTGGAGCCAGACTTAGGCACACAAATGCCACCA 1675
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1676 QY CCACAGTGTGCGGCACAAGCCGTCGGTAGGTATGTCTGAAATGAGCTCGGAG 1735
1577 Db CCACAGTGTGCGGCACAAGCCGTCGGTAGGTATGTCTGAAATGAGCTCGGAG 1636
1736 QY ATTGGCTCGCAC-CTGGAGCGAGATGGAAGCTTAAGGACGGCGGACAGGAAGATGCGAG 1794
1637 Db ATTGGCTCGCACGGCTGACGAGATGGAAGCTTAAGGACGGCGGACAGGAAGATGCGAG 1696
1795 QY GCAGCTGAGTTGTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGGGTGCTGTAA 1854
1697 Db GCAGCTGAGTTGTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGGGTGCTGTAA 1756
1855 QY CGGTGAGGCGCAGTGTAGTCTGAGCAGTACTCGTTGTCGCGCGCGCCACACAGACATA 1914
1757 Db CGGTGAGGCGCAGTGTAGTCTGAGCAGTACTCGTTGTCGCGCGCGCCACACAGACATA 1816
1915 QY ATAGCTGACAGACTAACAGACTGTTCTTTCATGGGTCTTTTCTGAGTCACTCGTCTGTC 1974
1817 Db ATAGCTGACAGACTAACAGACTGTTCTTTCATGGGTCTTTTCTGAGTCACTCGTCTGAA 1876
1975 QY GAC---GAATTCAGCAATCATGGATGCAATGAAGAGGGCTCTGCTGTGCTGCTG 2030
1877 Db TTCTCTAGCACTCGAAGCTTATGTCTTCAATGAAAGAAAGCTGGTCTAACAGATG 1936
2031 QY CTGTGTGGAGCAGTCTTCTGTTTCCGCCAGCGCTAGCGAAACCCACGTC-ACCGGGGGAAG 2089
1937 Db ACAACTAGAACAAAGGCGAGGCGCCATCTGCGGCCACGACTCAAAACGACAGATGCCA 1996
2090 QY TGGCGGCCACATGCTGTCTGGATTGTTAGCTCTCTCGCACAGGCGGCCAAGCAGAACGT 2149
1997 Db GGCCTTGAGCTTTTCGGGCTGGATCTCTGAGCAGCTAATGACCGGAAGAAATCTCTGAAGC 2056
2150 QY CCAGCTGATCAACACCAACGAGTTGGGACCTCAATAGCAGGCGCTGACTGCAATCA 2209
2057 Db GACATCTTCTGTGATATTGAGAAACAATCCAGGATTTATGCTAGCAGTCCCAATTCGACAA 2116
2210 QY TAGCCTCAACACCGGCTGTGGTGGCGGCTTTTCTATCACCAAGTCTCAACTCTTCAGG 2269
2117 Db ACGAAGCCAAACCGAAGACGCGCA---ACAGTCAAAACCAACGACCCCAATTTGCAAT 2173
2270 QY CTGTCTGAGAGCTAGCCAGCTGCGGACCCCTTACCGATTTTTCAGCAGGCTGGGGCCC 2329

2174 Db CATAGTTTGTAGG-----AGGTAGTACAAACATTTGGCTTCTATTTGGCTACTGTTGTGCAAC 2228
2330 QY TATCAGTTATGCAACGGAAGGGCGCCGACAGCGCCCTACTGCTGGCACTACCCCC 2389
2229 Db AACAAACCATCGATCAGAAATCATTTAGAACACGCAATTAGAGTCTTGAGAAATGGTCTAA 2288
2390 QY AAAACCTTCCGGTATTGTCCCGCGAAGAGTGTGTGGTCCGGTATATTGCTTCACTCC 2449
2289 Db AGCCAGTTTATGATATGGCAAAACAACTCTCCTCATTTGAACAGGGTTTGTGCTGAGATGG 2348
2450 QY CAGCCCGGTGGTGGGAACGACCGACAGGTGCGGGCGGCCACCTACAGCTGGGGTGA 2509
2349 Db TTGCAAAATATGATCTTCTGGTGTAGCAACCGGTGCGGCAACAGCAACCGCTGCGGCAA 2408
2510 QY AAATGATACGGAGCTCTTCGTCTTAAATAACAGGCGCACCGCTGGGCAATTTGGTTGCG 2569
2409 Db CTGAGG-----CTTATTTGGGCGGAACATGTTCAACACCTCGACATCACTTTAT 2461
2570 QY TTGTACTCGATGAACTCAACTGGATTCAACAAAGTGTGGAGCGCTCTCTTGTGTAT 2629
2462 Db GAAGAAAGTGCATTCGGGGTAAGATTGAATCTAGAGATGAGACCGTCC---TCAAAG 2517
2630 QY CAGAGGGCGGCAACCAACCTGCACTGCCCTCACTGATTTGCTTCGCAAGCATCGGA 2689
2518 Db TGTAGGGAGGCAATTCACAAATCTAAACAGTACCCT----- 2554
2690 QY CGCCACATACTCTCGTGGCGCTCGGTCCCTGGATCACACCGAGTGCCTGCTCGACTA 2749
2555 Db --TCACTAATCAGGAAATTTTGGGAAACCTTGACATTTTCGGCAAGGATTTGAGAAACA 2612
2750 QY CCCGTATAGCTTTGGCATTTATCTTTGTACCATCACTCACTACCATATTTAAATTCAGGAT 2809
2613 Db TTATGTATGATCACTTGCCTGGTTTGGAACTGCTTTTCCACCAATTTAGTACAGTATTT 2672
2810 QY GTAAGTGGAGGGGTGGAACACAGGCTGGAAGTGCCTCAACTGACGCGGGGCGAAG 2869
2673 Db GTAAATTTGGGAAAGATAGCAACTCATTTGGACATCATTTCACTGCTGAGTTTCCAGGCCAGCC 2732
2870 QY TTGCGATCTGGAAGATAGGACAGGTCGAGATCGATATGGAGAACATCACATCAGGATT 2929
2733 Db TGGCTGAGGAGACTCTCTCTCAATGTGCCCTTAATTTCAAAATTCACAAAGAGTTTCAATCT 2792
2930 QY CTTAGGACCCCTGCTCGTGTATTACAGCGGGGTTTTTTTGTGTGACAAGAAATCTCTCAAT 2989
2793 Db TCCAAAGATGCTCTCATCTGTATCCACATCGCTTTTCAGGTGACATTTCCCGAGCTT 2852
2990 QY ACCGACAGTCTAGACTCGTGTGGA-CTTCTCTCAATTTTCTAGGGGATCTCCCGTGT 3048
2853 Db GCCAGAAAGCTTGGTCCAGTCCACCATCGCCCAAGATTGATCGAGTTGGGATGTGT 2912
3049 QY GTCTTGGCCAAATTCG---CAGTCCCAACCTCCAATCACTCACCAACCTCTGCTCTC 3105
2913 Db TTTTCAGCTTCAAGATGTAAACACTTGGACTCAAAATTTGAGCCAAATCTCCCTTCCCT 2972
3106 QY CAATTTGCTCTGTTTATCGCTGGATGTGCTCGCGGTTTTTATCATATTTCTCTTCATCC 3165
2973 Db CGAAAGAGGCGAAATAATAGCAGAGGCTTCAACTGCTGAACATATAGGTACGTTACAT-- 3030
3166 QY TCGTGTATGCTCATCTTCTTATTTGTTTCTTCTGATTTATCAAGTATTTGTCGCCGTTT 3225
3031 Db -----TAATGATACACTTGTGAGTATCAGCCCTGGATAATTAAGTCAATTTAAACGACC 3084
3226 QY GTCTCTAATTCAGGATCAACAAACAGTACGGGACCATGCAAAACCTGCACGACTC 3285
3085 Db AAGATAAAATTTGTTTCAATCTCTGCTAGCAGCTTAAATATAAATGTAATGAGAGCTATAT 3144
3286 QY CTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGTGTTGTAACAAACCTACGATGGAATTT 3345
3145 Db CTCTGACAGGGGATCCAGATCTGCTGTGCTTCTAGTTGCCAGC----- 3189
3346 QY GCACTGTATTTCCCATCCCATCGTCTGGGCTTTTCGCAAAATACCTATCGGAGTGGGCTT 3405
3190 Db ---CATCTGTTGTTGGCCCTCCCGTGCCTTCTTGTGACCTGGAAGGTGCCACTCCCA 3246

Qy	3406	CAGTCCGCTTCT - CTTGGCTCAGTTTACTAGTGCCTATTGTTTCAGTGGTTCGTAGGGCTT	3464
Db	3247	CTGTCTCTTCTTAATAAAATCAGGAAATTCGATCGCATTTCTCTGAGTAGTGTCATTCTA	3306
Qy	3465	TCCCCCACTGTTTGGCTTTT	3524
Db	3307	TTCTGGGGGTGGGTGGGAGCAGCAGCAAGGGGGAGGATGTGGGAAGACAATAGCAGGC	3366
Qy	3525	AGCATCGTAGTCCCTTTATACCGCTGTTAACCAATTTTCTTTTGTCTCTCGGTATACATT	3584
Db	3367	ATGCTGGGATCGGTGGCTCTATGGGTACCCAGGTGCT - - - - - GAAGATTG	3415
Qy	3585	TAGAANTTCAGATTCGAGCAAGTCTGAAGGCGCGCAAGATATCAAGGATCCACTACG	3644
Db	3416	ACCGGTTCTCTCTGGGCCAAGAAAGCAGGACATCCCTCTTCTCTGTGACACACCCCTG	3475
Qy	3645	CGTTAGAGCTCGCTGATCAGCCTCGACTGTGCGCTTCTAGTTGTCAGGCCATCTGTTGTTTG	3704
Db	3476	TCACGCCCTTGTTTATGTTTCAGGCCCACTCATAGGACATCATAGCTCAGGAGGGC	3535
Qy	3705	CCCCCCCCCGTGCCTTCTTGACCTCTGGAAGGTGCCACTCCCACTGCTCTTCTTCTTAATA	3764
Db	3536	TCCGCTTCAATCCACCCGCTAAAGTACTTTGAGCGGTCTCTCCCTCCCTCATCAGCCC	3595
Qy	3765	AAATGAGGAATTCGATTCGCAATTGTCTGAGTAGTGTCATTCTATTCTGGGGGGTGGGT	3824
Db	3596	ACCAACCAAACTTAGCTTCCAAGAGTGGGAAGAAATAAAGCAAGATAGGCTATTAAAGT	3655
Qy	3825	GGGCGAGCAGCAAGGGG - - GAGGATTGGAAGACAATAGCAGGCATCCTCGGGAGCT	3881
Db	3656	GCAGAGGAGAGAAATGCCTCCACATGTGAGAGATATGAGAGAAATCATAGAAATT	3715
Qy	3882	CTTCCGCTTCTCGCTCACTGACTCGCTCGGCTCGGTCTGTTTCGGCTCGCGCAGCGGTAT	3941
Db	3716	CTTCCGCTTCTCGCTCACTGACTCGCTCGGCTCGGTCTGTTTCGGCTCGCGCAGCGGTAT	3775
Qy	3942	CAGTCTACTCAAAGGGCGTAAACGGTTATCCACAGAAATCAGGGGATAACGCAAGGAAGA	4001
Db	3776	CAGTCTACTCAAAGGGCGTAAACGGTTATCCACAGAAATCAGGGGATAACGCAAGGAAGA	3835
Qy	4002	ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTCTCGCGCT	4061
Db	3836	ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTCTCGCGCT	3895
Qy	4062	TTTTTCATAGGCTCCGCCCCCTTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGT	4121
Db	3896	TTTTTCATAGGCTCCGCCCCCTTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGT	3955
Qy	4122	GGCGAAACCGACAGGACTATAAGATAACAGGGGTTTCCCTTGGNAGCTCCCTGTGTC	4181
Db	3956	GGCGAAACCGACAGGACTATAAGATAACAGGGGTTTCCCTTGGNAGCTCCCTGTGTC	4015
Qy	4182	GCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAA	4241
Db	4016	GCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAA	4075
Qy	4242	CGGTGGCGCTTTCTCAATGTCAAGCTGTAGGTATCTCAGTTTCGGTGTAGGTCTGTGCT	4301
Db	4076	CGGTGGCGCTTTCTCAATGTCAAGCTGTAGGTATCTCAGTTTCGGTGTAGGTCTGTGCT	4135
Qy	4302	CCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGGACCGCTCGCCTTATCCGGTA	4361
Db	4136	CCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGGACCGCTCGCCTTATCCGGTA	4195
Qy	4362	ACTATCGCTTTAGTCCAAACCGGTAAAGACAAGCTTATCCCACTGGCAGCAGCCACTG	4421
Db	4196	ACTATCGCTTTAGTCCAAACCGGTAAAGACAAGCTTATCCCACTGGCAGCAGCCACTG	4255
Qy	4422	GTAAACAGGATTAACAGACGAGGTATGTTAGCGCGTGTCTACAGATTTCTGAAGTGTGGC	4481
Db	4256	GTAAACAGGATTAACAGACGAGGTATGTTAGCGCGTGTCTACAGATTTCTGAAGTGTGGC	4315

RESULT 6

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: Sequence 34. Application US/10491121

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: GENERAL INFORMATION:

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 : APPLICANT: NABEL, GARY

APPLICANT: NABEL, GARY
APPLICANT: YANG ZHI-YONG

; APPLICANT: YANG, ZHI-YONG

APPLICANT: SULLIVAN, NANCY
APPLICANT: SANCHEZ, ANTHONY

APPLICANT: SANCHEZ, ANTHONY

TITLE OF INVENTION:	DE
TITLE OF INVENTION:	F

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FILE REFERENCE: NIH221.001NP

; CURRENT APPLICATION NUMBER: US/10/491,12

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; NUMBER OF SEQ

; SOFTWARE:

; SEQ ID NO 34

; LENGTH:

TYPE: DNA

ORGANISM: A2

Query Match 40.2%; Score 2363; DB 18; Length 6259;
Best Local Similarity 70.6%; Pred. No. 0;
Matches 3498: Conservative 0; Mismatches 1280; Indels 177; Gaps 19;

Qy	1	TGCGCGTTTCGGTGATGACGGTGAACCTCTTGACACATGACAGCTCCCGAGACGGTCA	60
Db	1	TGCGCGTTTCGGTGATGACGGTGAACCTCTTGACACATGACAGCTCCCGAGACGGTCA	60
Qy	61	CAGCTTGTCTTAACCGGATCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAAGCGGTG	120
Db	61	CAGCTTGTCTTAACCGGATCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAAGCGGTG	120
Qy	121	TTGGCGGGTGTCCGGGCTGGCTTAATATGCGGCATCAGACAGATTGTACTGAGATGC	180
Db	121	TTGGCGGGTGTCCGGGCTGGCTTAATATGCGGCATCAGACAGATTGTACTGAGATGC	180

QY 181 ACATATGAAGCTTTTGGCAAAAGCCTAGGCTTCCAAAAAGCCTCCTCCTACTACTTCTGG 240
DB 181 ACCATATGCGG-----TGTGAATACCGCAC 207
QY 241 AATAGCTCAGAGCGAGGCGCTCGGCTCTGCATAAATAAAAAAATTAGTCAGCCA 300
DB 208 GATGCGTAAGGAGAAATAACCGCATCAG----- 235
QY 301 TGGGGCGGAGAAATGGCGGAACTGGCGGGGAGGAAATTAATGGCTTAATGGCCATTGCAAT 360
DB 236 -----ATTGGCTTAATGGCCATTGCAAT 256
QY 361 AGTTGTATCTATATCATTAATATGTACATTAATATTTGGCTCTATGTCCAATATGACGCCA 420
DB 257 ACGTTGTATCCATATCATTAATATGTACATTAATATTTGGCTCTATGTCCAATATGCGCCA 316
QY 421 TGTGACATTGATTAATGACTAGTTAATTAATAGTAATCAATTAACGGGTCATTAGTTCAAT 480
DB 317 TGTGACATTGATTAATGACTAGTTAATTAATAGTAATCAATTAACGGGTCATTAGTTCAAT 376
QY 481 AGCCCATATATGGAGTTCCGCGTTACATAAATTAACGGTAAATGGCCCGCTCGCTGACCG 540
DB 377 AGCCCATATATGGAGTTCCGCGTTACATAAATTAACGGTAAATGGCCCGCTCGCTGACCG 436
QY 541 CCCAACGACCCCGCCCATTTGACGTCAATTAATGACGTATGTTCCCATAGTAACGCCAATA 600
DB 437 CCCAACGACCCCGCCCATTTGACGTCAATTAATGACGTATGTTCCCATAGTAACGCCAATA 496
QY 601 GGGACTTTCANTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTA 660
DB 497 GGGACTTTCANTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTA 556
QY 661 CATCAAGTGTATCATATGCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGGGCC 720
DB 557 CATCAAGTGTATCATATGCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGGGCC 616
QY 721 GCTGGCAATATGCCAGTACATGACTTTACGGGACTTTTCTTATTTGGCAGTACATCTAC 780
DB 617 GCTGGCAATATGCCAGTACATGACTTTTATGGGACTTTTCTTATTTGGCAGTACATCTAC 676
QY 781 GTATTAGTATCGCTATTACCATGTTGATGGGTTTTGGCAGTACACCAATGGGGTGA 840
DB 677 GTATTAGTATCGCTATTACCATGTTGATGGGTTTTGGCAGTACATCAATGGGGTGA 736
QY 841 TAGCGGTTTGACTACGCGGATTTCCAAAGTCTCCACCCTTACGCTCAATGCGAGTTTG 900
DB 737 TAGCGGTTTGACTACGCGGATTTCCAAAGTCTCCACCCTTACGCTCAATGCGAGTTTG 796
QY 901 TTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCTGAATAACCCCGCCCGTTGACG 960
DB 797 TTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCTGAATAACCTCCGCCCATTTGACG 856
QY 961 CAAATGGGCGGTAGGCGTGTACGTTGGGAGTCTATATAAGCAGAGCTCGTTTATGTGAAC 1020
DB 857 CAAATGGGCGGTAGGCGTGTACGTTGGGAGTCTATATAAGCAGAGCTCGTTTATGTGAAC 916
QY 1021 CGTCAAGTCCCTGGAGAGCCATCCACGCTGTTTGGACCTCCATAGAAGACACCGGGAC 1080
DB 917 CGTCAAGTCCCTGGAGAGCCATCCACGCTGTTTGGACCTCCATAGAAGACACCGGGAC 976
QY 1081 CGATCCAGCTCCGCGCCCGGAAACGGTGTCAATTTGAAACCGGATTTCCCGTGGCCAAAGT 1140
DB 977 CGATCCAGCTCCGCGCCCGGAAACGGTGTCAATTTGAAACCGGATTTCCCGTGGCCAAAGT 1036
QY 1141 GACGTAAGTACCGCTATAGACTATATAGGACACCCCTTTGGCTCTTATGATGCTATA 1200
DB 1037 GACGTAAGTACCGCTATAGACTATATAGGACACCCCTTTGGCTCTTATGATGCTATA 1096
QY 1201 CTGTTTTTGGCTTTGGGCTTATACACCCCGC--TCCTTATGCTATAGGTGATGTTATAGC 1259
DB 1097 CTGTTTTTGGCTTTGGGCTTATACACCCCGCTTCTTATGCTATAGGTGATGTTATAGC 1156
QY 1260 TTAGCCTATAGGTGTTGGGTTATTGACCAATATTGACCACTCCCTTATTGGTGACGATACT 1319

DB 1157 TTAGCCTATAGGTGTTGGGTTATTGACCAATATTGACCACTCCCTTATTGGTGACGATACT 1216
QY 1320 TTCCATTAATTAATCATTAACATGGCTCTTTGGCCAACTATCTCTATTTCGCTATATGCCA 1379
DB 1217 TTCCATTAATTAATCATTAACATGGCTCTTTGGCCAACTATCTCTATTTCGCTATATGCCA 1276
QY 1380 ATACTCTGTCTTTACAGAGCTGACACGGACTCTGTATTTTACAGGATGGGT-CCATTT 1438
DB 1277 ATACTCTGTCTTTACAGAGCTGACACGGACTCTGTATTTTACAGGATGGGTCCCATTT 1336
QY 1439 ATTATTACAATTTACATATAAACAACCGCGCTCCCGTCCCGCTCCCGCACTTTTATATAA 1498
DB 1337 ATTATTACAATTTACATATAAACAACCGCGCTCCCGTCCCGCTCCCGCACTTTTATATAA 1396
QY 1499 CATAGCGTGGGATCTCC-----GACATCTCGGTACGTGTTCCGAGACATGGGCTCTTCTCG 1555
DB 1397 CATAGCGTGGGATCTCCCGGAACTCTCGGTACGTGTTCCGAGACATGGGCTCTTCTCG 1456
QY 1556 GTAGCGCGGAGCTTCCACATCCGAGCCCTGCTCCCATCCGCTCCAGCGCTCATGTGCG 1615
DB 1457 GTAGCGCGGAGCTTCCACATCCGAGCCCTGCTCCCATCCGCTCCAGCGCTCATGTGCG 1516
QY 1616 TCGGAGCTCTCTGCTCTTAACAAGTGGAGCCAGACTTTAGGCAACAGCAAAATGCCCA 1675
DB 1517 TCGGAGCTCTCTGCTCTTAACAAGTGGAGCCAGACTTTAGGCAACAGCAAAATGCCCA 1576
QY 1676 CCACAGTGTGCGGCACAAAGCGCTGGGTTAGGCTATGCTGCTGAAATAGCTCGGAG 1735
DB 1577 CCACAGTGTGCGGCACAAAGCGCTGGGTTAGGCTATGCTGCTGAAATAGCTCGGAG 1636
QY 1736 ATTTGGCTCGCAC-CTGGACGAGATGGAAGACTTTAAGGCGAGCGGAGAGATGCGAG 1794
DB 1637 ATTTGGCTCGCACGCTGACGAGATGGAAGACTTTAAGGCGAGCGGAGAGATGCGAG 1696
QY 1795 GCAGCTGATGTTGTTGTAATCTGATAAGAGTACAGGTAATCTCCGTTGCGGTGCTGTTAA 1854
DB 1697 GCAGCTGATGTTGTTGTAATCTGATAAGAGTACAGGTAATCTCCGTTGCGGTGCTGTTAA 1756
QY 1855 CGGTGGAGGCGAGTGTAGTCTGAGCAGTACTCGTTGCTGCGCGCGGCGGAGAGAGATTA 1914
DB 1757 CGGTGGAGGCGAGTGTAGTCTGAGCAGTACTCGTTGCTGCGCGCGGCGGAGAGAGATTA 1816
QY 1915 ATAGCTGACAGACTAAACAGACTGTTCTTTCATAGGCTCTTTCTGCACTACCGCTGTC 1974
DB 1817 ATAGCTGACAGACTAAACAGACTGTTCTTTCATAGGCTCTTTCTGCACTACCGCTGTC 1876
QY 1975 GACGAATTCAGCAATCATGGATG-ATGAAAGAGAGGCTCTGCTGTGTGTGCTG 2030
DB 1877 GACAGTGTGATCAGATATCGCGCGCTCTAGAAATTTAGGATTTGCGCTTTTAGAGATT 1936
QY 2031 CTGTGTGGAGCAGTCTTCTGTTTCGCGCCAGCTAGGAAACCCAGTCAACCGGGGAGT 2090
DB 1937 ACTACTAGTTAGGAATTTCTAAATCATGGGCGAGATTATTAATTTTCAAGAGTGGC 1996
QY 2091 GCGGCGCACACTGTGCTGTGATTGTTAGC-CTCCTCGCACCGGCGGCGGAGAGAGT 2149
DB 1997 ACATGTAATAGGGAAGTATGAAACATTTGTGCTAATTTGGCTTTCTTATTGGCAATCT 2056
QY 2150 CCAGTGTATCAACCAACGCGAGTTGGCACTCAATAGCAGCGGCTGAACTGCAATGA 2209
DB 2057 GAAAGGCTGTATAACATCGCTACATGTGGGATTTAGGATTTGGTGGTCTTTTATTCTTT 2116
QY 2210 TAGCCTCAACACCGCTGGTTGGCAGGCTTTCTATACCAAGATTTCACTCTCAGG 2269
DB 2117 GTGTGGCAAGTCTTGTTCCTAAACCTTAAAGGGGATATGAGCTGCAACCTTAGAAT 2176
QY 2270 CTGCTCAGAGGCTAGCCAGCTGCGACCTTACCGATTTTGAACGGGCTGGGGCC 2329
DB 2177 AATATAGGAGCCCTTAACATGACCATGCCCTTATCATGCAACCAAGAGAGTATCA 2236
QY 2330 T----ATCAGTTATGCAACGGAAGCGGCCCCGACCGGC-----CCCTACTGTGGCACTA 2383

Db 2237 TTACATAAGAGTGGGCAATGAGACTGGATTAGNATTGACTTTAACTAAACACAGCAATTAT 2296
QY 2384 CCCCCCAAAACCTTGGCGTATTGTGCCCGCAAGAGTGTGTGGTCCGGTATATTGCTT 2443
Db 2297 AAATCAAAAATTTTGGCAACTTATCCGATGCTCACAAAAAGAAATCTTTATGATCATGCTCT 2356
QY 2444 CACTCCAGCCCGTGGTGGGAGACGACGACGAGGTGGGGGGCCCACTACAGCTG 2503
Db 2357 CATGAGCATCATCTCAACATTCATCTATCCATTCCTCAATTCAGTATGAAGCCAT 2416
QY 2504 GGGTGAATGATACCGAGCTCTTCGTCCTTAACAAATACAGGCCACCGCTGGGCAATTG 2563
Db 2417 GAGTTGTGATTCATGAGGGAATCAATGAGTGCATACAACTCTCTCATTCCTATGC 2476
QY 2564 GTTCGGTTGATCTGGATGAATCACTAATCGGATTCACAAAGTTGCGGAGCCCTCTTGT 2623
Db 2477 TGGGGATCGGGCGGAACACTGTGGGACAGTTCGCAAGGAGTGTTCGCAAACTTTATGAG 2536
QY 2624 TGTCAATCGAGGGGGGCAACAAACCTGCACTGCTCCCACTGATGTTGTTCCGCAAGCA 2683
Db 2537 AATGGCTGGGGTGAAGATACATTTGATTCAGTACAGAAAGGGAACCTGGGACTGTAT 2596
QY 2684 TCCGAGCGCACATCTCTCGTGGGCTCCGGTCCCTGGATCACACCCAGGTGCTGCT 2743
Db 2597 AATGACCACTACCACTGATTAATCAAAATACAACTGGGAGGACACTGCCAATT 2656
QY 2744 CGACTACCGTATAGCTTTTG--CATTAATCTTTGATCCATCACTACCACTATTTAAA 2801
Db 2657 CTCAGACCGTCTCTATCGGTACCTTGGCCCTTTGTCAAAAGGACAAAGAGATATA 2716
QY 2802 ATCAGATGTAGTGGAGGGTGCAGACAGCTGGAAGCTGCCCTGCACTGGACGGG 2861
Db 2717 TATAAGTAGGAGCTCTTCGGGACCTTCAC-----CTGGCAATTTGTCAGATTCTG 2766
QY 2862 GCGCAAGTTGCGATCTGGAAGATAGGACAGTCCGAGATCGATATGAGAAACATCAC 2921
Db 2767 AGGGCAATGAACACCACTGATTTATTTAAACAGGTGGATGCTAATTTGAACGAGAC 2826
QY 2922 TCAGGATTCCTAGGACCCCTGCTCGTGTACAGGGGGGTTTTCTTTGTTGACAAAGATC 2981
Db 2827 TCAAGTGTTTTGGGAATACAGCTGTGGCAAAATGCAATGAGAAGCATGATGAGGAGTTT 2886
QY 2982 CTCAGATACCGAGATCTAGACTCGTGGTGAATCTCTCAATTTTCTAGGGGATCT 3041
Db 2887 GTGACATGTGAGATTTGTTGATTTCAAACAAGCAAGCAATCCGTAGTTGAAGGCTGAG 2946
QY 3042 CCGGTGTGTTGGCCAAAATTCGAGTCCCAACCTCCAACTCACTCAACCACTCTCTGT 3101
Db 2947 CCAGATGAGTATCAATTAATAATAAGCCGTGATGCTGATCAATGATCAATTA 3006
QY 3102 CTCCA-----ATTGTCTCGTTATCGCTGGATGTGTCTGGCGGTTTTAT 3148
Db 3007 TCATGAAGAACCAATTAAGAGACATCATGGGCAATCCCTACTGCAATTAACAGCAAGTAT 3066
QY 3149 CATATTCTCTCATCTGCTGCTATGCTCTCTCTTTATTTGGTTCCTTCTGATTAACA 3208
Db 3067 GGTACCTTAATCATACTAGTAGGGGGAACATCACTACAAAGTTGTGGCTTTATATCCA 3126
QY 3209 AGGTATGTTGGCGGTTTGTCTTAATTCAGGATCAACAAACAGTACGGGACCAATG 3268
Db 3127 ATGGGTCAATCTAATTAAGAACCCAGTCTCTGTGATGACATAGAACAGCAAGCAATA 3186
QY 3269 CAAAACCTGCAGACTCTG-----CTCAAGGCAACTCTATGTTTCCCTCATGTT 3318
Db 3187 TGATCACAGAGATGCTTCAGAAAGAAATACATTAAGAGACAGGGAACCGCCCTGTAGG 3246
QY 3319 GCTGTACAAAACCTACGATGGAATTGC---ACCTGATTTCCCATCCCATCGTCTGGG 3375
Db 3247 GATCCAGATCTGCTGTGCTCTCTAGTTGCGAGCCATCTGTGTTGGCCCTCCCGCTGC 3306
QY 3376 CTTTTCGAAAATACCTATTCGGAGTGGGCTCAGTCCGTTTCT--CTTGGCTCAGTTTACTA 3434
Db 3307 CTTCTTGACCTGGNAGGTGCCACTCCCACTGTCTTTCTTAATAAATAGGAAATTG 3366

QY 3435 GTGCCAATTTGTTCACTGGTTCGTAGGGCTTTCCCCCACTGTTTGGCTTTCACTATATGG 3494
Db 3367 CATCGCAATTTCTGAGTAGGTCTCAATTTCTCTGGGGGTGGGTGGGCGAGGACAGCA 3426
QY 3495 ATGATGTGTAATTTGGGGCCCAAGTCTGTACAGCATCTGTAGTCCCTTTATATACCGCTGTTA 3554
Db 3427 AGGGGAGGATTTGGGAAGACAAATAGCAGCATGCTGGGGATCGGTTGGCTCTATGGGTA 3486
QY 3555 CCAATTTTCTTTTG---TCTCTGGGTATACATTTAAGAAATTCAGACTCGAGCAAGCTAG 3611
Db 3487 CCCAGGTCTGAAGAAATTTGACCCGTTCTCTCGGGCCAGAAAGAGCAGGACACATCCCC 3546
QY 3612 AAAGGGCGCCAAAGATATCAAGGATCCACTAGCGCTTTAGAGTCCGCTGATACGCTCGAC 3671
Db 3547 TTCTCTGTGACACACCTGTCCACGCCCTGGTTCTTAGTTCCAGCCCCACATCATAGGAC 3606
QY 3672 -----TGTGCCCTTTAGTTGTCAGGCATCTGTTGTTTTCGCCCTCCCGTGGC 3719
Db 3607 ACTCATAGTCTAGGAGGGTCCGCTTCAATCCCAACCCGCTAAAGTACTTTGGAGCGTCT 3666
QY 3720 TTCTCTTGACCTTGAAGGTGCCACTCCCACTGCTCTTCTTAATAAAATGAGAAATTGC 3779
Db 3667 CTCCCTCCCTCATCAGCCCAACCAAACTAGCTCCAAAGATGGGAAGAAATTA 3726
QY 3780 ATCGCAATTTGTCTGAGTAGTGTCTATCTATTCTGGGGGTGGGTGGGACGACAGCA 3839
Db 3727 GCAAGATAGGCTATTAAAGTGCAGAGGAGAGAAAATGCTCCAACTGTGAGGAGATAT 3786
QY 3840 GGGGAGGATTTGGGAAGACAATAGCAGCATCTCGGGAGCTCTTCGCTTCTCGCTCA 3899
Db 3787 GAGAAATCATAGAAATTTTAAAGCCCATG--GCCTTAATCTTCGCTTCTCGCTCA 3844
QY 3900 CTGACTCGCTGCGCTCGGTTCGGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGG 3959
Db 3845 CTGACTCGCTGCGCTCGGTTCGGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGG 3904
QY 3960 TAATACGGTTATTCACAGAAATCAGGGATTAACGAGGAAAGAAACATGTGAGCAAAAGCC 4019
Db 3905 TAATACGGTTATTCACAGAAATCAGGGATTAACGAGGAAAGAAACATGTGAGCAAAAGCC 3964
QY 4020 AGCAAAAGCCAGGAAACCGTAAAGGCGGCTCTCGCGCTTTTTCATAGGCTCCGCG 4079
Db 3965 AGCAAAAGCCAGGAAACCGTAAAGGCGGCTCTCGCGCTTTTTCATAGGCTCCGCG 4024
QY 4080 CCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 4139
Db 4025 CCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 4084
QY 4140 TATAAAGATACAGGGGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCC 4199
Db 4085 TATAAAGATACAGGGGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCC 4144
QY 4200 TGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAAT 4259
Db 4145 TGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT 4204
QY 4260 GCTCACTGCTGATAGTATCTCAGTTCCGTTAGTTCGTTTCGCTCCAAGCTGGGCTGTGTC 4319
Db 4205 GCTCACTGCTGATAGTATCTCAGTTCCGTTAGTTCGTTTCGCTCCAAGCTGGGCTGTGTC 4264
QY 4320 AGGAACCCCGCTTACAGCCCGACCGCTGGCTTATCCGTTAACTATCGTCTTGAGTCCA 4379
Db 4265 AGGAACCCCGCTTACAGCCCGACCGCTGGCTTATCCGTTAACTATCGTCTTGAGTCCA 4324
QY 4380 ACCCGGTAAAGACACCACTTATCGCACTGGGACGACCACTGTAACAGGATTTAGCAGAG 4439
Db 4325 ACCCGGTAAAGACACCACTTATCGCACTGGGACGACCACTGTAACAGGATTTAGCAGAG 4384
QY 4440 CGAGGTATGTAGGCGGTGCTACAGAGTTCTTTGAAGTGTGGCTTAACCTACGCTACACTA 4499
Db 4385 CGAGGTATGTAGGCGGTGCTACAGAGTTCTTTGAAGTGTGGCTTAACCTACGCTACACTA 4444

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QY 4500 GAAGGACAGATTTGGTATCTGGCTCTGCTGAGCCAGTTACCTTCGGAAAAAGAGTTG 4559
DB 4445 GAAGAACAGTATTTGGTATCTGGCTCTGCTGAGCCAGTTACCTTCGGAAAAAGAGTTG 4504
QY 4560 GTAGCTCTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGTTTTTTTGGTTCAGC 4619
DB 4505 GTAGCTCTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGTTTTTTTGGTTCAGC 4564
QY 4620 AGCAGATTAGCGCGCAGAAAAAAGGATCTCAAGAAGATCTTTTGATCTTTTCTACGGGT 4679
DB 4565 AGCAGATTAGCGCGCAGAAAAAAGGATCTCAAGAAGATCTTTTGATCTTTTCTACGGGT 4624
QY 4680 CTGACGCTCAGTGAACGAAACCTCAGCTTTAAGGATTTTGGTCATGAGATTATCAAAA 4739
DB 4625 CTGACGCTCAGTGAACGAAACCTCAGCTTTAAGGATTTTGGTCATGAGATTATCAAAA 4684
QY 4740 GGATCTCAGCTAGATCTTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 4799
DB 4685 GGATCTCAGCTAGATCTTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 4744
QY 4800 ATGAGTAAACTTGGTCTGACAGTTTACCAATGCTTAAATCAGTGAAGGACCTTCTCAGCG 4859
DB 4745 ATGAGTAAACTTGGTCTGACAGTTTACCAATGCTTAAATCAGTGAAGGACCTTCTCAGCG 4804
QY 4860 TCTGCTATTTCGTTTCATCCATAGTTGCTGACTC 4894
DB 4805 TCTGCTATTTCGTTTCATCCATAGTTGCTGACTC 4839
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RESULT 7

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US-10-763-976A-14
; Sequence 14, Application US/10763976A
; Publication No. US20050026288A1
; GENERAL INFORMATION:
; APPLICANT: Harms, Jerome S
; APPLICANT: Splitter, Gary A
; APPLICANT: Bakle, Kurt A
; APPLICANT: Bremel, Robert D
; TITLE OF INVENTION: Inducible Protein Expression System
; FILE REFERENCE: 2240/3
; CURRENT APPLICATION NUMBER: US/10763, 976A
; CURRENT FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 7685
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Engineered Sequence from virus and plasmid
; FEATURE:
; NAME/KEY: LTR
; LOCATION: (149)..(737)
; OTHER INFORMATION: 5' MoMuSVLTR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1753)..(2148)
; OTHER INFORMATION: Blasticidin Resistance
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (2257)..(3074)
; OTHER INFORMATION: CMV IE promoter
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (3078)..(3102)
; OTHER INFORMATION: attB1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3115)..(4041)
; OTHER INFORMATION: BLV Tax
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: (4046)..(4070)
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; OTHER INFORMATION: attB2
; FEATURE:
; NAME/KEY: misc signal
; LOCATION: (4082)..(4674)
; OTHER INFORMATION: WPRE; woodchuck hepatitis virus post-transcriptional regulatory
; OTHER INFORMATION: element
; FEATURE:
; NAME/KEY: LTR
; LOCATION: (4720)..(5313)
; OTHER INFORMATION: 3' MoMuSVLTR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6616)..(7476)
; OTHER INFORMATION: Ampicillin Resistance
US-10-763-976A-14

Query Match 39.6%; Score 2331; DB 19; Length 7685;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 3704; Conservative 0; Mismatches 1665; Indels 184; Gaps 19;

QY 337 ATTATTTGGCTATTGGCCATTTCGCATACGTTGCTATCTATATCATATATGTACATTATATT 396
DB 2301 AATATTTGGCTATTGGCCATTTCGCATACGTTGCTATCTATATCATATATGTACATTATATT 2360
QY 397 GGCTCATGTCCCAATATGACCGCCATGTTGACATTTGATTTATTTGACTAGTTATTAATAGTAA 456
DB 2361 GGCTCATGTCCCAATATGACCGCCATGTTGACATTTGATTTATTTGACTAGTTATTAATAGTAA 2420
QY 457 TCAATTTACGGGGTCATTTAGTTTCATAGCCCATATATGAGAGTTCCGCGTTACATACCTTACG 516
DB 2421 TCAATTTACGGGGTCATTTAGTTTCATAGCCCATATATGAGAGTTCCGCGTTACATACCTTACG 2480
QY 517 GTAAATGGCCCGCTCGCTGACCGCCCAAGACGCCGCCCATGAGCTCAATTAATCAACG 576
DB 2481 GTAAATGGCCCGCTCGCTGACCGCCCAAGACGCCGCCCATGAGCTCAATTAATCAACG 2540
QY 577 TATGTTTCCCATAGTAAACGCAATAGGAGACTTTCCATTGACGTCAATGGGTGGAGTATTTA 636
DB 2541 TATGTTTCCCATAGTAAACGCAATAGGAGACTTTCCATTGACGTCAATGGGTGGAGTATTTA 2600
QY 637 CGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCAAGTCCGCCCTTATT 696
DB 2601 CGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCAAGTCCGCCCTTATT 2660
QY 697 GAGCTCAATGACGGTAAATGGCCCGCTGCGCATTTATGCCAGTACATGACCTTACGGGAC 756
DB 2661 GAGCTCAATGACGGTAAATGGCCCGCTGCGCATTTATGCCAGTACATGACCTTATGGGAC 2720
QY 757 TTTCTTACTTTGGCAGTACATCTACGTATTAGTATGCTATGCTATTAACCATGGTATCGCGTTT 816
DB 2721 TTTCTTACTTTGGCAGTACATCTACGTATTAGTATGCTATTAACCATGGTATCGCGTTT 2780
QY 817 TGGCAGTACACCAATCGGCGTGATAGCGGTTTGTGACTCAGCGGATTTTCCAGTCTCCAC 876
DB 2781 TGGCAGTACATCAATCGGCGTGATAGCGGTTTGTGACTCAGCGGATTTTCCAGTCTCCAC 2840
QY 877 CCCATTGAGTCAATCGGAGTTTGTGTCACCAAAATCAACGGGACTTTTCCAAATGT 936
DB 2841 CCCATTGAGTCAATCGGAGTTTGTGTCACCAAAATCAACGGGACTTTTCCAAATGT 2900
QY 937 CGTAAATAACCCCGCCCGTTGACGAAATGGGCGGTAGGCGTGTACGGTGGGAGTCTAT 996
DB 2901 CGTAAACAATCCCGCCCGTTGACGAAATGGGCGGTAGGCGTGTACGGTGGGAGTCTAT 2960
QY 997 ATAAGCAGAGCTCGTTTGTAGTGAACCGTCAAGATCGCTGGAGACGCCATCCACGCTGTTTT 1056
DB 2961 ATAAGCAGAGCTCGTTTGTAGTGAACCGTCAAGATCGCTGGAGACGCCATCCACGCTGTTTT 3020
QY 1057 GACCTCCATAGAGACACCGGGACCCATCCAGCTCCGCGCGGGGACCGTGCATTGGA 1116
DB 3021 GACCTCCATAGAGACACCGGGACCCATCCAGCTCCGCGCGGGGACCGTGTGTTTACACA 3080
QY 1117 ACGGGATTTCCCGCTGC - CAAGAGTGACGTAAAGTACCGCTATAGACTCTATAGGCACAC 1175
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Db 3081 AGTTTGTACAAAAAGCAGCTCCCGCGCCACCATGGCAAGTGTGTGGTGGGGCC 3140
QY 1176 CCCTTTGGGCTCTTATGACGTACTACTGTTTGGCTTGGGCTATACACCCCGCTCC 1235
Db 3141 CCACTCTTACATGCTCGCGGCCCTGGTTTGTCCAATGATGTCAACATCGATGC--- 3197
QY 1236 TTATGCTATAGGTATGGTATAGCTTAGCCTATAGGTGTGGGTATTATGACCATTTATGAC 1295
Db 3198 -----CTGGTGGCCCTCTCGCGGCCCCATGAGCGACTCCAAATTCGAAAGGATCGAC 3249
QY 1296 CACTCCCTTATGGTGACCATCTTTCATTACTAATTAATCAATAGGCTCTTTGGCCACA 1355
Db 3250 AACAGCTCACCTG---CGAGACCCACCGTATCAACTGGACCGCCGATGGACGACCTTGC 3306
QY 1356 ACTATCTCTATTGGCTATATGCCNACTCTGTCTTTCAGAGACTGACACGGAATCTGTA 1415
Db 3307 GGCCTCAATGGAACTGTGTCTCGACTGCATGTCTCGAGACCCGCGCCCA----- 3359
QY 1416 TTTTACAGATGGGTCCATTATTATTTTACAAATTCACATATACAAAGCCGCTCC 1475
Db 3360 -----AGGGCCCGCGGTTCACTTTCCTTCGAGCGGTCCCG-----CTTCAAGCCCTACCA 3409
QY 1476 CCGTGCCCGCAGTTTTTATTAACATAGCGTGGATCTCGACATCTCGGTTACGTTTC 1535
Db 3410 AGCCCGCGCGGTTTCACTTTCCTTCGAGCGGTCCCG-----CTTCAAGCCCTACCA 3464
QY 1536 CGACATGGGCTCTTCTCGGTAGCGCGGAGCTTCCACATCCGAGCCCTGTGCCATCC 1595
Db 3465 ATGCCAATTTGCCCTCGGCTCTAGCGAGGTTCGCCCATTTACGGGACGCGCTTCTTCC 3524
QY 1596 GTCCAGCGCTCATGTCTCGTGGAGCTCTTGTCTTCAACAGTGGAGGCCAGACTTAG 1655
Db 3525 CTGGAACTAGTAAAGCATCTCTCTCAGAAAAGTCTTATATTAAATCAATGGC 3584
QY 1656 GCACAGCAATATGCCACACACACAGTGTGGCGACAGGCGGTGGGTAGGTATGT 1715
Db 3585 CAATTTTTCTTACTCCCTCTTCGATACCTCTTGTGGACCCCTCGGCTGTCCGT 3644
QY 1716 GTCTGAAATAGCTCGGAGTTGGCTCGCACCTGGAGCGAGATGGAAGACTTAAGGCA 1775
Db 3645 CTTTGGCCCGACACACAGGGAGCCATAGTTATCTCTCACCTTTTGAAGCTATGCC 3704
QY 1776 GCGGAGAAAGATGAGGAGCTGAGTTGTGTATTTCTGATAGAGTCAAGGTAACT 1835
Db 3705 GGCTACTTGTATTTCACTACCCCTAGCGAGCGCTTCTCTCTAATGTCCCATATGCCGCTT 3764
QY 1836 CCGTTTGGGTGTGTAAACGGTGGAGGCGAGTGTAGTCTGAGCAGTACTCGTTGCTGCC 1895
Db 3765 TCCCGGGACTCAATGAACCCCTTTCAGAAITTCGAGTGCCTTATTCGAAACGCC 3824
QY 1896 GCGCGGCCACACAGATAATAGCTGACAGACTA--ACAGACTGTCTCTTTTCCATGGTCT 1953
Db 3825 CGGCTGTCTTGTCTGTCCCCGGATCGACCTATTCTTAAACGGTCCCCCTTCCCATG 3884
QY 1954 TTTTCTGCACTCACCGTCTGACGAATTCAGCAATCATGGATGCAATGAAGAGAGGCG 2013
Db 3885 CGACCGTTTACAGTATGTGTCCAGTCTCAGGCTTACAGCGCTTCTCTCATGACCCTAC 3944
QY 2014 TCTGCTGTGTGCTGTGTGGAGCAGTCTTCTGTTTCGCCCGCGCTAGGGAACCC 2073
Db 3945 GCTAACCTGGTCGGAATAGTGTCTAGCAGAAAAATAAGACTTGAATTCCTCCCTTAAAT 4004
QY 2074 AGTCAACCGGGGAAGTGGCGGC-CACACTGTGTCTGGATTTTGTAGCCCTCTTCGACCA 2132
Db 4005 ACAACTGCTAGAAAATGAATGGCTCTCCCGCTTTTGTGAGACCCAGCTTCTTGTACAA 4064
QY 2133 GGGCCCAAGAGAACTGCAGCTGATCAACCAACGCGAGTTGGCAGCTTCAATAGCAG 2192
Db 4065 AGTGTGTATAACATCATCAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGT 4124
QY 2193 GGCCTCAACTGCAATGATAGCTCAACACCGGCTGTGGAGGCTTTTCTATCAACCAC 2252

Db 4125 ATTCTTAACATATGTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCTTTGTAT 4184
QY 2253 AAGTTCAACTCTTACGGCTGTCTCTGAGAGGTAGCCAGTCCGACCCCTTACCAGATTT 2312
Db 4185 CATGCTATTGCTTCCGTATGCTTCAATTTCTCTCTCT-TGTATAAATCTCTGGTTGCT 4243
QY 2313 GACCAGGCTGGGCGCTATCAGTTATGCCAAGGAGGCGGCCGACAGCGCCCTAC 2372
Db 4244 GTCTCTTTATAGGAGTTGTGCCCCGTGTCAAGCAACGTGGCTGGTGTGCACTGTGT 4303
QY 2373 TCGTGCACCTACCCCAAAACCTTGCCTGTTATGTGCCCGCGCAAGAGTGTGTGTGCTCG 2432
Db 4304 TCGTAGCGAACCCCT--ACTGTTGGGCAATGCCACCACTGTGAGCTCTTTTCGGG 4361
QY 2433 GTATATTGCTTCACTCCAGCCCGGTGTGGGAAACGACACAGGTGCGGCGCGCC 2492
Db 4362 ACTTTGCTTCCCTCTCTATTTGCCACGGCGAACTCATGCCGCTGCCCTTGGCCGC 4421
QY 2493 ACCTACAGCTGGGTGAAAATGATACGAGCTTCTTGTCTTAACAATACAGGCCACCG 2552
Db 4422 TCGTAGACAGGGG-----CTCGGCTGTGGGCACTGACAAATTCGCTGGTGTG 4469
QY 2553 CTGGGCAATTGCTCGGTTGTACCTGGATGAACCTCAACTGGATTACACAAAGTGTGGGA 2612
Db 4470 TCGGGAAATCATCGTCTTCTTGGCTGTGCTGTGTGCCACCTGGATTCTGGCG 4529
QY 2613 GCGCTCTTGTGTCACTCGAGGGCGGGCAACAACCCCTGCATGCCCCCACTGATTC 2672
Db 4530 GGGAGCTCTTCTGTCTACGTCTTCCGCTTCAATCAGCGGACCTTCTTCCCGCGC 4589
QY 2673 TTCGCAAGCATCCGAGCGCACATCTCTCGTGGGCTCCGCTCCCTGGATCACACC 2732
Db 4590 CTGCTGCCGCTCTCGGCTCTTCCGCTTTCGCTTCGCTTCAGACGAGTCGGATC 4649
QY 2733 AGTGGCTCTGCTCGACTACCCGTATAGCTTTCGCTTATCTGTATACCATCAACTACAC 2792
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QY 2793 ATATTAAATCAGGATGTAAGTGGAGGGGTGCAACAACAGGTGGAAGCTGCTGCAAC 2852
Db 4710 AAAAGGGGGAATGAAGACCCCACTGTAGGTTTGGCAAGCTAGCTTAAGTAAACCCAT 4769
QY 2853 TGGACGCGGGGCAAGCTTGGATCTGGAAGATAGGACAGGTCCGAGATCGATATGGAG 2912
Db 4770 TTTGCAAGCATGGAAAAATAATACTGAGAATAGAGAAGTTTCAATCAAGTCAAGAA 4829
QY 2913 AACATCACATCAGGATTTCTAGGACCCCTGCTCGTGTACAGCGGGGTTTTTCTTGTG 2972
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QY 2973 ACAAGAACTCTCACAAATACCGCAGAGTCTAGACTCGTGTGGAGCTTCTCTCAATTTCTA 3032
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QY 3033 GGGGATCTCCGCTGTCTTGGCCAAATTCGAGTCCCAACCTCCATCACTCACCA 3092
Db 4950 GCAGTTCCTTCCCGGCTCAGGGCCAAAGAACAGTGGTCCCCAGATGC----- 4997
QY 3093 ACTCTCTGCTCCAAATTTGTCTGTTATCGTGTGATGTCTGCGCGTTTTTATCAT 3152
Db 4998 -GGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTG----- 5046
QY 3153 TTCCTCTTCATCCTGCTGATGCTCTCATCTTTCTTATGTTCTTCTGGATTTATCAAGGT 3212
Db 5047 -----CCCCAAGGACCTGAAATGACCTGTGCTTATTGAACTAACCAATCAGTTCGCT 5101
QY 3213 ATGTTGCCGTTGCTCTCTAATTCAGGATCAACAACAACAGTACGGGACCATGCATA 3272
Db 5102 TCTCGCTCTGTTCG----- 5119
QY 3273 ACTGCAACGACTCTGCTCAAGCAACTCTATGTTTCCCTCATGTTGTGTGTACAAACCT 3332
Db 5120 GCTTCTGCTCCCGAGCTCAATAAAGAGCCCAACACCCCTCCTCCTCGGGGCGCAGTCT 5179


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Db 7284 GAAAAGCTTCTTCGGGGGGAAGAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTGGA 7343
Qy 5550 TGTAACCCACTCGTGTGACCCAACTGATCTTTCAGCATCTTTTACTTTTCAACAGGGTTTCTG 5609
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Db 7644 ATAAAAATAGCGCTATCACGAGGCCCTTTTCGTC 7676

RESULT 8
US-10-401-000-2
; Sequence 2, Application US/10401000
; Publication No. US20040038304A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert D.
; APPLICANT: Bakle, Kurt
; APPLICANT: Imboden, Michael
; TITLE OF INVENTION: Antibody Libraries
; FILE REFERENCE: GALA-07886
; CURRENT APPLICATION NUMBER: US/10/401,000
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 60/368,808
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/371,299
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 7626
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-401-000-2

Query Match 39.5%; Score 2321.4; DB 17; Length 7626;
Best Local Similarity 67.4%; Pred. No. 0;
Matches 3744; Conservative 0; Mismatches 1566; Indels 243; Gaps 24;

Qy 337 ATTAATGGCTATTGGCCATTGTCATAGCTTGTATCTATATCATTAATATGACATTTATATT 396
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Qy 397 GGCTCATGTCCAATATGACCGCCATTGTGACATTTATGATGATTTATGATTTATTAATAGTAA 456
Db 2361 GGCTCATGTCCAATATGACCGCCATTGTGACATTTATGATGATTTATGATTTATTAATAGTAA 2420
Qy 457 TCAATTTACGGGGTCATTAGTTTCATAGCCCATATATGAGTTCCGCGTTACATAACTTACG 516
Db 2421 TCAATTTACGGGGTCATTAGTTTCATAGCCCATATATGAGTTCCGCGTTACATAACTTACG 2480
Qy 517 GTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCAATGACGTCATAATGACG 576
Db 2481 GTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCAATGACGTCATAATGACG 2540
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Qy 577 TATGTTCCCATAGTAACGCCAATAGGAGCTTTCCATTGAGCTCAATGGGTGGAGTATTTA 636
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Qy 697 GACGTCATGACGGTAAATGGCCCTGGCAATTTATGCCAGTACATGACCTTACGGGAC 756
Db 2661 GACGTCATGACGGTAAATGGCCCTGGCAATTTATGCCAGTACATGACCTTATGGGAC 2720
Qy 757 TTTCTCTACTTTCGACAGTACATCTACGTTATGATCATCGCTATTACCATGCTGATCGGTTT 816
Db 2721 TTTCTCTACTTTCGACAGTACATCTACGTTATGATCATCGCTATTACCATGCTGATCGGTTT 2780
Qy 817 TGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAAGTCTCCAC 876
Db 2781 TGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAAGTCTCCAC 2840
Qy 877 CCATTTGACGTCATAGGGAGTTTGTGTCACCAAAATCAAACGGGACTTTTCCAAATGT 936
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Qy 997 ATAAGCAGAGCTCGTTTGTAGTGAACCGTCAGATCGCTCGGAGAGCGCCATCCAGCTGTTTT 1056
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Qy 1177 CTTTGGCTCTTATGATGATCTATCTGTTTGGTGTGGGGCTATACACCCCGCTCCT 1236
Db 3141 ACCATGGGATGAGCTGTATCATCTCTCTTTGG-TAGCAACAGCTTACAGGTGTCACATC 3199
Qy 1237 TATGCTATAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1296
Db 3200 CGAGGTCCAACTGCTGGAGAGCGGTGG--AGGTGTTGTGCAACCTGGCCGGTCCCTGGCG 3257
Qy 1297 ACTCCCTATTGTTGAGCATGATCTTTCCATTACTTAATCCATACATGGCTCTTTGCCACAA 1356
Db 3258 CTGTCCTGCTCCGCTCTGCTGCTTGGCTTTCGATTTCAACATATTTGGATGATGATGATGATGAT 3317
Qy 1357 CTATCTCTATGGCTATATGCCAATCTCTGCTCTTCAGAGACTGACACGGACTCTGTAT 1416
Db 3318 GCACCTGGAAAAGGCTCT-----TGAGTGGATTTGAGAAAATTCATCCAGATAGCAG 3367
Qy 1417 TTTTACAGGATGGGGTCCATTTATTTATTTACAAAATTCATATACAAACAGCCGCTCCCG 1476
Db 3368 TAGCAATTAATGATGCGCCGCTCTTAAAGGATAGATTTACAATATATCGCA--GACAAACGCC 3425
Qy 1477 CGTGCCCGAGTTTATTTAAACATAGCGTGGATCTCCGACATCTCCGGTACGCTGCTCC 1536
Db 3426 AGAAACATATGTTCTCGCAATTTGACAGCTTGAGACCCGAAAGACACCGGGGTCTATTTT 3485
Qy 1537 GGACATGGGCTCTTCTCCGCTAGCGGCGAGCTTCCATCCGAGCCCTGGTCCCATCCG 1596
Db 3486 TGTGCAAGCTTTACTTCCGCTTCCCTGTTGCTTTATTTGGGGCAAGGACCCCGGTC 3545
Qy 1597 TCCAGGGGCTCATGTTGCTGCGTCCGAGCTCTTCTCTCTTAAAGTGGAGGCGAGACTTAG 1656
Db 3546 ACCGTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCTTGGCACCTCTCTCTCAAG 3605
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[illegible]

Db	4589	AGCTTTCTTGTA	CAAAAGTGGTGATA	-----ACATCGATAA	AAATAAAGATT	4634				
Qy	2793	ATATTTAAAAAT	CAGGATGTACGT	GGGAGGGT	CGAAACACAGAGCT	TGGAAAGCTCGCTGCAAC	2852			
Db	4635	TTATTTAGTCT	TCAGAA	AAAGGGGNA	TGAAGACCCCA	-CTGTAGGTTTGGCAAGCT	4693			
Qy	2853	TGACCGCGGG	CGAAACGTT	CGCATCT	TGGAAGATAGGGACAGG	TCCGAGATCGATATGCGAG	2912			
Db	4694	AGCTTAAGTA	AACGCCATTTT	TGCAAGGCAT	TGAAAAATACATA	ACTGAGA	-----ATAGAG	4748		
Qy	2913	AACATCACAT	CACAGATTCCT	AGGACCCCT	GCTCGTGTACAGGGGGTTTTT	TCTGTTGTTG	2972			
Db	4749	AGGTT	CAGATCAAGGT	-----	-----CAGGAAC	CAGATGGAACAGCTG	4785			
Qy	2973	ACAAGAAT	CCTCACAAT	TACCGCAGAGT	CTAGACTCGTGGTGGATCT	CTCTCAATTTTTCTA	3032			
Db	4786	AAATATGGG	CAAAACAGGATAT	CTGTGGTA	GACAGTTCTCCTCCCGGCT	CAGGGCCAGAA	4845			
Qy	3033	GGGGGATCT	CCCCGTGTCT	TGGCCAAAAT	TGCAAGTCCCCAA	CCCTCAA	TA	CTCACTCA	3092	
Db	4846	CAGATGGAA	CAGCTGAATAT	TGGCCAAA	CAGGATATCTGTGGT	TAAGCAGTTCTCTGCCCCG	4905			
Qy	3093	ACCTCTGT	CCTCAATTTGT	CTCGTTAT	TCGCTGGATGTCT	TGGGCGCTTTAT	TCATA	3152		
Db	4906	GCTCAGGG	CCAAGAACAGAT	TG3TCCC	CAGATGGGTCC	CAGCCCTCAG	CAGTTTCTAGAGA	4965		
Qy	3153	TTCTCTT	TCATCTGTCT	GCTATG	CGCTCATCTTCTTAT	TGGTCTCTCTGGAATTA	CAAGGT	3212		
Db	4966	ACCATCAG	TGTTTCAGGGT	GC	CCCAAGACCTGA	ATGACCTGTGT	GCCTTATTTGAAC	5025		
Qy	3213	ATGTGCGC	GTTTGTCTCT	TAA	TTCAGGATCAAC	CAACACAGTACGGG	ACCA	TGCAAA	3272	
Db	5026	TAACCAAT	CAGTTTCGCTT	CTCGTTC	TGCGCGCTTCTGTCT	CCCGAGCTCA	ATAA	5085		
Qy	3273	ACCTGCAG	AGTCTCTGCT	CAAGGCAACT	CTATGTTTCCCTCAT	TGTGCTGTATCA	AAACCT	3332		
Db	5086	AGAGCCCA	CAACCCCTCACT	CGGGGGCCAGT	CTCCGATTTGAT	TGACTGAGT	CGCCGGGTAC	5145		
Qy	3333	ACGGATG	GAATATGCACCTGT	ATTTC	CCATCCATCGTCTGGGCTT	TCGCAAAATACCTA	3392			
Db	5146	CCGTGTAT	CAATAAACCCTCT	TGAGTTCGAT	TCCAGCTTGTGGTCTCGC	-----	5195			
Qy	3393	TGGGAGT	TGGCCCTCAGT	CCGTTTCTCT	TGGCTCAGT	TTTACTAGT	TGCCATTTGT	CAGTGG	3452	
Db	5196	-----	-----TGTTCT	CTGGAGGGTCT	CTCTGAGT	TGATTGACT	ATCCCG	5235		
Qy	3453	TTCGTAGGG	CTTCCCCCACTG	TTTGGCTTTAC	GTATATATG	ATATGAT	TGATGTGGTAT	TGGGG	3512	
Db	5236	TCAGCGGG	-----	GTCTTTTCAT	TTTTTTCAT	TGGGGGCTCGT	CCGGGATCGGG	5283		
Qy	3513	CCAAGT	CTGTACAGCAT	CGTGAGT	CTCCTTTAT	ACCCTGT	TACCAATTTTCT	TTT---GT	3569	
Db	5284	AGACCCCT	TGCCAGGAC	CAACCCAC	CCACCGGGAGT	TAAGCTGGCT	GCCTCGCGCGT	5343		
Qy	3570	CTCTGGT	TATACATTTAA	GAATTTACAG	ACTCGAGCAAGT	CTAGAAAGCG	CGCCAAAGATAT	3629		
Db	5344	TTCGGTGA	TGACCGGTG	AAACCTCT	GA	CATG	CAGCTCCCGG	NACGGTCA	CAGTTGT	5403
Qy	3630	CAAGGAT	TCCACTACGGCT	TAGAGCTCGCT	GTATCAG	CGCTCGACTGT	GCTTCT	TAGTTGCCA	3689	
Db	5404	CTGTAAG	CGGATGCCGG	GAGCAG	-----	-----ACAAG	CCCGT	CAGGGCGC	5444	
Qy	3690	GCCATCT	GTGTGTTGGCCCT	CCCCCGTCT	CCTTGAC	CCCTGGAAAGGT	GCCACTCC	CCAC	3749	
Db	5445	GT	CAGCGGGT	TGCGGGGTGT	CGGGGGCAG	CCATGAC	CCAGT	TAGCATAGCGG	5504	
Qy	3750	TGTCTCT	TTCTTAATA	AAAAATGAG	GAATTTGAT	CGCATTTGTCT	CAGTAGGTGT	CAATTTCTAT	3809	
Db	5505	AGTGTAT	-----	-----ACTGG	CTTA	ACTATGCGGCAT	CAGACGAT	TGTAC	5547	
Qy	3810	TTCTGGGGGT	TGGGTGGGG	CAGGAC	CAAGG	GGGAGGATTTGG	GAAGACA	CAATAGCAGGCA	3869	

Db 5548 TGAGAGTGACCATATATGCGGTGTGAATACCGCACAGATGCGTAAGAGGAGAAATACCGCA 5607
Qy 3870 TGGTGGGAGCTCTTCCGCTTCTCGCTCACTGACTGCTGCGCTCGGTGCTGCTGC 3929
Db 5608 ---TCAGGGCGCTCTTCCGCTTCTCGCTCACTGACTGCTGCGCTCGGTGCTGCGCTGC 5664
Qy 3930 GCGGAGCGGTATCAGCTCACTCAAGAGCGGTAAATACGGTTTCCACAGAAATCAGGGGATA 3989
Db 5665 GCGGAGCGGTATCAGCTCACTCAAGAGCGGTAAATACGGTTTCCACAGAAATCAGGGGATA 5724
Qy 3990 ACCAGAGAAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCCGTAAAAAGCGCG 4049
Db 5725 ACCAGAGAAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCCGTAAAAAGCGCG 5784
Qy 4050 CGTTGCTGGCGTTTTCATPAGGCTCCGCCCTCCCTGACGAGCATCAAAAAATCGACGCT 4109
Db 5785 CGTTGCTGGCGTTTTCATPAGGCTCCGCCCTCCCTGACGAGCATCAAAAAATCGACGCT 5844
Qy 4110 CAAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGCGTTTCCCTCGGAA 4169
Db 5845 CAAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAAGCGTTTCCCTCGGAA 5904
Qy 4170 GCTCCCTCGTGCCTCTCTGTTCCGACCTGCGGCTTACCGGATACCTGTCCGCCCTTTC 4229
Db 5905 GCTCCCTCGTGCCTCTCTGTTCCGACCTGCGGCTTACCGGATACCTGTCCGCCCTTTC 5964
Qy 4230 TCCCTTCGGGAAGCGTGGCGCTTTCATATGCTCACGCTGTAGGTATCTCAGTTCGGGT 4289
Db 5965 TCCCTTCGGGAAGCGTGGCGCTTTCATATGCTCACGCTGTAGGTATCTCAGTTCGGGT 6024
Qy 4290 AGGTGCTTCCGCTCAAGCTGGGCTGTGCAAGAACCCCGTTCAGCCGACCGCTCGG 4349
Db 6025 AGGTGCTTCCGCTCAAGCTGGGCTGTGCAAGAACCCCGTTCAGCCGACCGCTCGG 6084
Qy 4350 CTTTATCCGCTAACTACTGTTTGGCTCAACCCCGTAAAGACACGACTTATCGCCACTGG 4409
Db 6085 CTTTATCCGCTAACTACTGTTTGGCTCAACCCCGTAAAGACACGACTTATCGCCACTGG 6144
Qy 4410 CAGACGCCACTGGTAAACAGGATPAGCAGACGAGGTATGAGCGGTGCTACAGAGTTCT 4469
Db 6145 CAGACGCCACTGGTAAACAGGATPAGCAGACGAGGTATGAGCGGTGCTACAGAGTTCT 6204
Qy 4470 TGAAGTGGTGGCTAACTACGCTACACTAGAGGACAGTATTTGGTATCTCGCTCTGC 4529
Db 6205 TGAAGTGGTGGCTAACTACGCTACACTAGAGGACAGTATTTGGTATCTCGCTCTGC 6264
Qy 4530 TGAAGCAGTTTACCTTTCGGAAGAGTGGTAGCTCTTGTATCCGCGCAACCAACCCG 4589
Db 6265 TGAAGCAGTTTACCTTTCGGAAGAGTGGTAGCTCTTGTATCCGCGCAACCAACCCG 6324
Qy 4590 CTGGTACCGGTGGTTTTTTTGGTTTGAAGCAGAGATTAACGCGCAAGAAAGGATCTC 4649
Db 6325 CTGGTACCGGTGGTTTTTTTGGTTTGAAGCAGAGATTAACGCGCAAGAAAGGATCTC 6384
Qy 4650 AAGAAGATCTTTTGTATCTTCTACCGGCTGACGCTCAGTGGACGAAACTCAGCTT 4709
Db 6385 AAGAAGATCTTTTGTATCTTCTACCGGCTGACGCTCAGTGGACGAAACTCAGCTT 6444
Qy 4710 AAGGATTTTGGTCATGAGATTAACAAAGGATCTTCACTAGATCTTTTAAATTTAA 4769
Db 6445 AAGGATTTTGGTCATGAGATTAACAAAGGATCTTCACTAGATCTTTTAAATTTAA 5504
Qy 4770 AATGAAGTTTAAATCAATCAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAAT 4829
Db 6505 AATGAAGTTTAAATCAATCAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAAT 6564
Qy 4830 GCTTATCAGTGGGACCACTATCTCAGCGATCTGTCTATTTCTTCTCATCATAGTTGCT 4889
Db 6565 GCTTATCAGTGGGACCACTATCTCAGCGATCTGTCTATTTCTTCTCATCATAGTTGCT 6624
Qy 4890 GACTCCCGCTGGTGTAGATAAATACGATACGGGAGGCTTACCATCTGGCCCCAGTGTG 4949
Db 6625 GACTCCCGCTGGTGTAGATAAATACGATACGGGAGGCTTACCATCTGGCCCCAGTGTG 6684

Qy 4950 CAAATGATACCGCGAGACCCACGCTCACCGCTCCAGATTATCAGCAATAAACACGACGAG 5009
Db 6685 CAAATGATACCGCGAGACCCACGCTCACCGCTCCAGATTATCAGCAATAAACACGACGAG 6744
Qy 5010 CCGGAAGGCCGAGCGAGAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTAA 5069
Db 6745 CCGGAAGGCCGAGCGAGAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTAA 6804
Qy 5070 ATTGTTGCGGGAAGCTAGAGTAAGTAGTTCCCAAGTTAATAGTTTGCACAAGTTGTTG 5129
Db 6805 ATTGTTGCGGGAAGCTAGAGTAAGTAGTTCCCAAGTTAATAGTTTGCACAAGTTGTTG 6864
Qy 5130 CAATTGCTACAGGCATCGTGGTGTACGCTCGTGGTTGGTATGSGTTTCAATCAGCTCG 5189
Db 6865 CCAATTGCTGACGCACTCGTGGTGTACGCTCGTGGTTGGTATGSGTTTCAATCAGCTCG 6924
Qy 5190 GTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGTTAGCT 5249
Db 6925 GTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGTTAGCT 6984
Qy 5250 CCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTATCACTCATGGTTA 5309
Db 6985 CCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTATCACTCATGGTTA 7044
Qy 5310 TGGCAGCAGTGCATTAATTTCTTACTGTATGCCATCCGTAAGATGCTTTCTGTGACTG 5369
Db 7045 TGGCAGCAGTGCATTAATTTCTTACTGTATGCCATCCGTAAGATGCTTTCTGTGACTG 7104
Qy 5370 GTGAGTACTCAACCAAGTCAATTCGAGAAATAGTATGCGCGACCCGAGTGTCTTGGC 5429
Db 7105 GTGAGTACTCAACCAAGTCAATTCGAGAAATAGTATGCGCGACCCGAGTGTCTTGGC 7164
Qy 5430 CGGCGTCAATACGGGATAATACCGGCCACATPAGCAGAACTTTAAAGTGTCTCATCTG 5489
Db 7165 CGGCGTCAACCGGATAATACCGGCCACATPAGCAGAACTTTAAAGTGTCTCATCTG 7224
Qy 5490 GAAAAGTTCCTTGGGGGCAAACTCTCAGAGATCTTACCGCTGTGAGATCCAGTTCCA 5549
Db 7225 GAAAAGTTCCTTGGGGGCAAACTCTCAGAGATCTTACCGCTGTGAGATCCAGTTCCA 7284
Qy 5550 TGTAAACCACTCGTGACCCAACTGATCTTACGCACTCTTTTACTTTTACCAGCGTTCTG 5609
Db 7285 TGTAAACCACTCGTGACCCAACTGATCTTACGCACTCTTTTACTTTTACCAGCGTTCTG 7344
Qy 5610 GGTGAGCAAAAAACAGGAAGGCAAAATGCGCGCAAAAAAGGAATAAGGGCGACACGAAAT 5669
Db 7345 GGTGAGCAAAAAACAGGAAGGCAAAATGCGCGCAAAAAAGGAATAAGGGCGACACGAAAT 7404
Qy 5670 GTTGAATCTCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5729
Db 7405 GTTGAATCTCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 7464
Qy 5730 TCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAATAGGGGTTCCGCGCA 5789
Db 7465 TCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAATAGGGGTTCCGCGCA 7524
Qy 5790 CATTTTCCCGAAAAAGTGCCACTGACGTCTAAGAAACCAATTTATTCATGACATTAACCT 5849
Db 7525 CATTTTCCCGAAAAAGTGCCACTGACGTCTAAGAAACCAATTTATTCATGACATTAACCT 7584
Qy 5850 ATAAAAATAGGCGTATCAGAGCGCTTTCTGTC 5882
Db 7585 ATAAAAATAGGCGTATCAGAGCGCTTTCTGTC 7617

RESULT 9
US-10-401-000-1
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; Publication NO. US2004003804A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert D.
; APPLICANT: Bakle, Kurt

Qy	2197	TGA	A	C	T	G	C	A	A	T	G	A	T	A	G	C	T	C	A	A	C	C	G	G	T	G	T	T	G	G	C	A	G	G	C	T	T	T	C	T	A	C	A	C	A	A	-	G	2255
Db	4063	C	A	A	A	G	C	C	G	G	G	A	G	G	A	G	C	A	A	C	A	G	C	A	G	C	A	C	G	T	A	C	C	G	T	C	T	C	A	C	C	G	T	C	C	4122			
Qy	2256	T	T	C	A	A	C	T	T	T	C	A	G	S	T	C	T	G	A	G	A	G	S	T	A	G	C	T	G	C	C	A	G	C	C	T	T	A	C	G	A	T	T	T	G	A	2315		
Db	4123	T	G	C	A	C	A	G	A	G	A	T	G	G	C	A	A	G	T	A	C	A	A	G	T	A	C	A	A	G	T	C	T	C	A	A	C	A	A	A	G	C	C	T	C	4182			
Qy	2316	C	A	G	G	C	T	G	G	G	C	C	T	A	T	A	G	C	A	A	C	G	A	A	G	C	G	C	C	C	A	C	A	G	C	C	C	C	C	T	A	C	T	G	C	2375			
Db	4183	C	A	G	C	C	C	A	T	C	G	A	A	A	C	C	A	T	C	C	A	A	G	C	A	A	G	G	C	A	G	C	C	C	C	G	A	A	C	A	C	A	G	T	G	4242			
Qy	2376	T	G	S	C	A	T	A	C	C	C	C	C	A	A	A	C	T	T	G	C	C	G	G	A	A	G	T	G	T	G	T	G	C	C	G	2433												
Db	4243	A	C	A	C	C	T	G	C	C	C	C	A	T	C	C	G	G	A	G	A	T	A	C	C	A	A	G	A	C	A	G	T	C	A	C	C	T	G	C	T	G	4302						
Qy	2434	T	A	T	A	T	G	C	T	T	C	A	C	C	C	C	C	T	G	T	G	T	G	G	A	C	G	A	C	G	A	C	T	G	C	C	C	C	C	C	C	C	C	2493					
Db	4303	T	C	A	A	G	G	C	T	C	T	A	T	C	C	A	G	C	A	C	A	T	C	C	C	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4348				
Qy	2494	C	C	T	A	C	A	G	C	T	G	G	T	G	A	A	T	G	A	T	A	C	G	A	C	G	T	C	T	T	C	G	T	C	T	T	A	C	A	A	T	A	C	A	G	C	C	2553	
Db	4349	T	G	G	C	A	G	C	C	G	A	A	C	A	A	C	A	C	A	G	C	C	T	C	C	G	T	G	T	G	A	C	T	C	C	A	C	C	A	G	C	T	C	T	4408				
Qy	2554	T	G	G	C	A	A	T	T	G	T	T	C	G	T	T	A	C	T	G	G	A	T	G	A	A	C	T	C	A	A	C	T	G	A	T	T	C	A	A	A	G	T	G	C	G	A	2613	
Db	4409	C	T	T	C	T	A	T	A	G	A	G	T	C	A	C	C	T	G	A	C	A	G	A	G	C	A	G	A	G	C	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	4459		
Qy	2614	G	C	C	T	C	T	T	G	T	C	A	T	C	G	A	G	G	G	C	G	G	A	C	A	A	C	C	C	T	G	C	A	C	T	G	C	A	C	T	G	A	T	G	C	2673			
Db	4460	C	G	T	C	T	C	A	T	G	C	T	G	A	T	G	A	C	A	G	G	C	T	T	G	C	A	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	G	A	G	C	4519
Qy	2674	T	C	C	A	G	A	C	T	C	G	A	C	A	T	A	C	T	C	T	C	G	T	C	G																								

3273	Qy	AC	TG	CAG	CAG	C	T	C	T	G	T	C	A	G	C	A	C	T	A	T	G	T	T	C	C	T	C	A	T	G	T	C	T	A	A	A	C	T	3333
5077	Db	AG	AC	CC	CA	CA	AC	CC	C	T	C	A	C	T	G	G	G	G	C	C	A	G	T	C	C	C	G	A	T	G	A	C	T	A	G	T	C	5136	
3333	Qy	AC	CG	AT	G	G	AA	T	T	G	C	A	C	T	G	A	T	T	C	C	A	T	C	C	C	A	T	C	G	T	G	G	C	T	T	C	G	3392	
5137	Db	CC	G	T	A	T	C	A	A	CC	C	T	C	T	T	G	C	A	G	T	T	G	C	A	T	C	C	A	A	A	T	A	C	C	T	A	5186		
3393	Qy	TG	G	A	G	T	G	G	C	C	T	C	A	G	T	T	T	C	T	C	T	G	G	C	T	T	A	C	T	A	G	T	T	A	C	T	3452		
5187	Db	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	5226				
3453	Qy	T	T	C	G	T	A	G	G	C	T	T	T	G	G	C	T	T	A	C	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	3512		
5227	Db	T	C	A	C	G	G	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	5274				
3513	Qy	C	C	A	G	T	C	T	A	C	A	G	C	T	T	A	C	C	G	T	T	A	T	A	C	C	G	T	T	A	C	A	A	T	T	3569			
5275	Db	A	G	A	C	C	C	T	G	C	C	A	G	A	C	C	A	C	C	G	G	A	G	T	A	A	G	T	A	A	G	T	A	A	G	5334			
3570	Qy	C	T	C	G	G	T	A	T	A	A	A	T	T	C	A	G	A	C	T	C	G	A	C	A	A	G	T	C	T	A	A	A	A	A	A	3629		
5335	Db	T	T	C	G	T	A	T	A	A	A	C	T	C	T	A	C	A	T	G	C	A	T	C	C	C	G	A	G	C	G	T	C	A	C	A	5394		
3630	Qy	C	A	A	G	A	T	C	A	C	G	G	T	A	G	A	C	T	C	G	T	G	A	T	C	A	G	A	C	T	G	C	T	T	A	G	3689		
5395	Db	C	T	A	A	G	C	G	A	T	G	C	G	A	G	A	C	A	G	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	5435			
3690	Qy	G	C	A	T	C	T	G	T	T	T	G	C	C	C	T	C	C	T	T	G	A	C	C	T	T	G	A	C	C	T	G	A	A	G	T	3749		
5436	Db	G	T	C	A	G	C	G	G	T	T	G	G	C	G	G	T	G	C	G	C	G	C	A	T	A	G	C	C	A	G	T	A	G	C	A	5495		
3750	Qy	T	G	T	C	T	T	C	T	A	A	A	A	T	T	G	A	G	A	A	T	T	G	C	A	T	T	G	C	A	T	T	G	T	C	A	3809		
5496	Db	A	G	T	A	T	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	5538				
3810	Qy	T	C	T	G	G	G	G	T	G	G	G	C	A	G	A	C	A	G	A	A	G	G	A	G	A	T	T	G	G	A	A	A	A	A	A	3869		
5539	Db	T	G	A	G	T	G	C	A	C	A	T	A	T	G	C	G	T	G	A	A	T	A	C	C	G	C	A	C	A	G	A	T	A	C	C	5598		
3870	Qy	T	G	T	G	G	G	A	C	T	T	C	G	C	T	C	A	C	T	G	A	C	T	G	C	T	G	C	C	T	G	C	T	G	C	T	3929		
5599	Db	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	5655			
3930	Qy	G	G	C	A	G	C	G	T	A	C	A	G	C	G	T	A	T	A	C	G	T	T	A	T	C	C	A	G	A	A	T	A	C	A	3989			
5656	Db	G	G	C	A	G	C	G	T	A	C	A	G	C	T	A	C	G	T	T	A	T	A	C	G	T	T	A	T	A	C	A	G	A	A	5715			
3990	Qy	A	C	G	A	A	A	A	C	A	T	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	4049			
5716	Db	A	C	G	A	A	A	A	A	C	A	T	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	5775			
4050	Qy	C	G	T	T	G	C	G	T	T	T	C	A	T	A	G	C	T	C	G	C	C	C	C	C	C	T	G	A	C	A	A	A	A	A	4109			
5776	Db	C	G	T	T	G	C	G	T	T	T	C	A	T	A	G	C	T	C	G	C	C	C	C	C	C	C	T	G	A	C	A	A	A	A	5835			
4110	Qy	C	A	G	T	C	A	G	A	G	T	C	G	A	A	C	C	C	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	4169			
5836	Db	C	A	A	G	T	C	A	G	A	G	T	C	G	A	A	C	C	C	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	5895			
4170	Qy	G	C	T	C	C	T	C	G	T	C	T	T	G	T	T	C	C	A	C	C	T	G	T	T	A	C	C	G	A	T	A	C	T	T	4229			
5896	Db	G	C	T	C	C	T	C	G	C	T	C	T	T	C	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	5955			
4230	Qy	T	C	C	T	T	G	G	A	C	G	T	T	T	C	T	C	A	A	T	G	C	A	C	G	T	A	T	C	A	G	T	T	C	G	T	4289		
5956	Db	T	C	C	T	T	G	G	A	A	C	G	T	T	T	C	T	C	A	T	A	G	C	T	A	G	T	A	T	C	T	C	A	G	T	T	6015		
4290	Qy	A	G	T	C	G	T	C	C	A	A	C	T	G	G	G	T	G	T	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	4349			
6016	Db	A	G	T	C	G	T	C	C	A	A	C	T	G	G	G	T	G	T	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	6075			
4350	Qy	C	C	T	A	T	C	C	G	G	T	A	C	T	T	T	A	G	T	T	C	C	A	A	C	C	C	G	T	A	A	G	A	C	A	C	4409		

[illegible]

Db	7156	CGGCGTCAACACGGGATAAATACCGCGCCACATAGCAGAACTTTTAAAGTGCTCATCAATTG	7215
Qy	5490	GAATAACGTTCTTTCCGGGCGAAAACTCTCAAGAGTCTTTACGCTGTGTGAGATCCAGTTTCGA	5549
Db	7216	GAATAACGTTCTTTCCGGGCGAAAACTCTCAAGGATCTTACCGCTGTGTGAGATCCAGTTTCGA	7275
Qy	5550	TGTAACCCACCTCGTGACCCCACTGATCTTTCAGCATCTTTTACTTTTACCAGAGCGTTTCTG	5609
Db	7276	TGTAACCCACCTCGTGACCCCACTGATCTTTCAGCATCTTTTACTTTTACCAGAGCGTTTCTG	7335
Qy	5610	GGTGAGCAAAAAACAGGAAGCAAAATCCGCAAAAAAGGGAATAAGGGCGACACGCGAAAT	5669
Db	7336	GGTGAGCAAAAAACAGGAAGCAAAATCCGCAAAAAAGGGAATAAGGGCGACACGCGAAAT	7395
Qy	5670	GTTGAATACTCATACTCTCTCTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT	5729
Db	7396	GTTGAATACTCATACTCTCTCTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT	7455
Qy	5730	TCATGAGCGGATACATATTTGAATGTATTAGAAAAATAAACAAATAGGGGTTCCCGCGCA	5789
Db	7456	TCATGAGCGGATACATATTTGAATGTATTAGAAAAATAAACAAATAGGGGTTCCCGCGCA	7515
Qy	5790	CATTTCCCGAAAAAGTGCACCTGACGCTCTAAGAAACCATTTATTCATGACATTAACTT	5849
Db	7516	CATTTCCCGAAAAAGTGCACCTGACGCTCTAAGAAACCATTTATTCATGACATTAACTT	7575
Qy	5850	ATAAAATAGGCGTATCACGAGGCCCTTTTCGTC	5882
Db	7576	ATAAAATAGGCGTATCACGAGGCCCTTTTCGTC	7608

RESULT 10

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US-10-359-120-50
; Sequence 50, Application US/10359120
; Publication No. US20040033487A1
; GENERAL INFORMATION:
; APPLICANT: NABLE, Gary J.
; APPLICANT: CHAKRABARTI, Bimal K.
; APPLICANT: HUANG, Yue
; TITLE OF INVENTION: MODIFICATIONS OF HIV Env, Gag, AND Pol
; TITLE OF INVENTION: ENHANCE IMMUNOGENICITY FOR GENETIC IMMUNIZATION
; FILE REFERENCE: NIH206.001C1
; CURRENT APPLICATION NUMBER: US/10/359,120
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: PCT/US01/25721
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/279,257
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/252,115
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/225,097
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 6577
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid pVR1012x/s containing HIV genes
US-10-359-120-50

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Query Match	38.9%;	Score	2290.6;	DB	17;	Length	6577;
Best Local Similarity	68.9%;	Pred. No.	0;				
Matches	3636;	Conservative	0;	Mismatches	1139;	Indels	502;
Gaps	16;						

Qy	1	TCGCGCGTTTCGGTGATGACGGTGAAACCTCTGACACATGACGCTCCCGAGACGGTCA	60
Db	1	TCGCGCGTTTCGGTGATGACGGTGAAACCTCTGACACATGACGCTCCCGAGACGGTCA	60
Qy	61	CAGCTTGTCGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGCTACGGGGTG	120
Db	61	CAGCTTGTCGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGCTACGGGGTG	120

QY	121	TTGGCGGGTGTGCGGGCTGGCTTAACTATGCGGCATCAGAGCAGATGTACTGAGAGTGC	180	1201	CTGTTTTTGGCTTGGGGCCTATACACCCCGC--TCCTTATGCTATAGGTGATGGTATAGC	1259
DB	121	TTGGCGGGTGTGCGGGCTGGCTTAACTATGCGGCATCAGAGCAGATGTACTGAGAGTGC	180	1097	CTGTTTTTGGCTTGGGGCCTATACACCCCGCTTCTTATGCTATAGGTGATGGTATAGC	1156
QY	181	ACCATATGAAGCTTTTGTGAAAAGCCTAGGCCTCCAAAAAGCCTCCTCACTACTTCTGG	240	1260	TTAGCCTATAGGTGTGGGTATTGTGACCCTATTTGACCCTATTCGGTGACGATACT	1319
DB	181	ACCATATGGG-----TTGGAATACCGCAC	207	1157	TTAGCCTATAGGTGTGGGTATTGTGACCCTATTTGACCCTATTCGGTGACGATACT	1216
QY	241	AATAGCTCAGAGCGCAGGGCGCTCGGCCTCTGCATAAATAAAAAAATTTAGTCAGCCA	300	1320	TTCCATTACTAATCCATAACATGGCTCTTTGGCAAACTATCTTATTTGGCTATATGCCA	1379
DB	208	GATGCGTAGGAGAAAATACCGCATAG-----	235	1217	TTCCATTACTAATCCATAACATGGCTCTTTGGCAAACTATCTTATTTGGCTATATGCCA	1276
QY	301	TGGGCGGAGAAATGGGCGGAATCGGCGGGAGGGAATTTATGGCTATTGGCCATTGCAAT	360	1380	ATACTCTGCTTTCAGAGACTGACAGGACTCTGTATTTTACAGAGTGGGT--CCATTT	1438
DB	236	-----ATTGGCTATTGGCCATTGCAAT	256	1277	ATACTCTGCTTTCAGAGACTGACAGGACTCTGTATTTTACAGAGTGGGTCCCATTT	1336
QY	361	ACGTTGTATCTATATCATATATGTACATTTATATTGGCTCATGTCCCATATGACGCCA	420	1439	ATTATTACAAATTCACATATACAAACGCGCTCCCCGCTGCCCGCAGTTTTTATATAA	1498
DB	257	ACGTTGTATCCATATCATATATGTACATTTATTTGGCTCATGTCCCATATGACGCCA	316	1337	ATTATTACAAATTCACATATACAAACGCGCTCCCCGCTGCCCGCAGTTTTTATATAA	1396
QY	421	TGTTGACATTTGATTGACTAGTTATTAATAGTAATCAATTAACGGGGTCATTAGTTTCAT	480	1499	CATAGCGTGGGATCTCC--GACATCTCGGGTA CGTGTTCGGGACATGGGCTCTTCTCG	1555
DB	317	TGTTGACATTTGATTGACTAGTTATTAATAGTAATCAATTAACGGGGTCATTAGTTTCAT	376	1397	CATAGCGTGGGATCTCCACGCGAACTCTCGGGTACGTGTTCGGGACATGGGCTCTTCTCG	1456
QY	481	AGCCCATATATGAGTTTCGCGTTACATAACTTACGGTAAATGGCGCGCTGGCTGACCG	540	1556	GTAGCGGCGGAGCTTCCACATCCGAGCCTGGTCCCATCCGTCAGCGGCTCATGGTCG	1615
DB	377	AGCCCATATATGAGTTTCGCGTTACATAACTTACGGTAAATGGCGCGCTGGCTGACCG	436	1457	GTAGCGGCGGAGCTTCCACATCCGAGCCTGGTCCCATCCGTCAGCGGCTCATGGTCG	1516
QY	541	CCCAACGACCCCGCCATTTGACGTCAATTAAGCTATGTCCCATAGTAAAGCCCAATA	600	1616	TCGGCAGCTCTTGTCTCTAACAGTGGAGCCAGACTTTAGGCACAGCAAAATGCCACCA	1675
DB	437	CCCAACGACCCCGCCATTTGACGTCAATTAAGCTATGTCCCATAGTAAAGCCCAATA	496	1517	TCGGCAGCTCTTGTCTCTAACAGTGGAGCCAGACTTTAGGCACAGCAAAATGCCACCA	1576
QY	601	GGGACTTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACATTTGGCAGTA	660	1676	CCAACAGTGTGCGGCAAAAGCGCGTGGGTAATGTCTGAAATAGCTCGGAG	1735
DB	497	GGGACTTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACATTTGGCAGTA	556	1577	CCAACAGTGTGCGGCAAAAGCGCGTGGGTAATGTCTGAAATAGCTCGGAG	1636
QY	661	CATCAAGTGTATCATATGCGCAAGTTCGCGCCCTTATTGAGCTCAATGACGGTAAATGGCCC	720	1736	ATTGGGCTCGCACCTG--GACGCAGATGGAGACTTTAAGCAGCGGCAGAGAGATGCAG	1794
DB	557	CATCAAGTGTATCATATGCGCAAGTTCGCGCCCTTATTGAGCTCAATGACGGTAAATGGCCC	616	1637	ATTGGGCTCGCACCTG--GACGCAGATGGAGACTTTAAGCAGCGGCAGAGAGATGCAG	1696
QY	721	GCCTGGCATATGCCAGTACATGACTTACGGGACTTTCTTACTTTGGCAGTACATCTAC	780	1795	GCAGCTGAGTGTGTATTCTGATAAGAGTCAAGGTAACTCCCGTTGCGGTGCTGTTAA	1854
DB	617	GCCTGGCATATGCCAGTACATGACTTACGGGACTTTCTTACTTTGGCAGTACATCTAC	676	1697	GCAGCTGAGTGTGTATTCTGATAAGAGTCAAGGTAACTCCCGTTGCGGTGCTGTTAA	1756
QY	781	GTATTAGTCACTCGCTATTACCATGGTGTATGCGGTTTTTGGCAGTACACCAATGGCGGTGA	840	1855	CGGTGAGGCGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCGCGCGCGCCACAGACATA	1914
DB	677	GTATTAGTCACTCGCTATTACCATGGTGTATGCGGTTTTTGGCAGTACATCAATGGCGGTGA	736	1757	CGGTGAGGCGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCGCGCGCGCCACAGACATA	1816
QY	841	TAGCGGTTTGACTCAACGGGATTTCCAAAGTCTCCACCCCAATGACGTCAATGGGAGTTTG	900	1915	ATAGCTGACAGACTAACAGACTGTTCTTCCATGGGTCTTTTCTGACGTCAACCGTCGTC	1974
DB	737	TAGCGGTTTGACTCAACGGGATTTCCAAAGTCTCCACCCCAATGACGTCAATGGGAGTTTG	796	1817	ATAGCTGACAGACTAACAGACTGTTCTTCCATGGGTCTTTTCTGACGTCAACCGTCGTC	1876
QY	901	TTTTTGGCACCAAAATCAACGGGACTTTCCAAATGTGTAATTAACCCCGCCCGTTGACG	960	1975	GAAGAAATCAAGCA--ATCATGGATGCAATGAAGAGAGGGCTCTGCTGTGCTGCTGC	2031
DB	797	TTTTTGGCACCAAAATCAACGGGACTTTCCAAATGTGTAATTAACCCCGCCCGTTGACG	856	1877	GACACGTGTATCAGATATCGCGCGCTCTAGACACCATGCGCGTGAAGGAGAACTACC	1936
QY	961	CAAAATGGCGGTAGGCGGTGTACGGTGGGAGGTCTATATAGCAGAGCTCGTTTATGTGAAC	1020	2032	TGTGTGGAGCAGTCTTTCGTTTCGCGCAGCGCTAGCGGAAACCCACGTCACCGGGGGAAGTG	2091
DB	857	CAAAATGGCGGTAGGCGGTGTACGGTGGGAGGTCTATATAGCAGAGCTCGTTTATGTGAAC	916	1937	AGCACCTGTGGCGCTGGGGCTGGCGCTGGGGACCACTGCTGTGGGCATGCTGATGATCT	1996
QY	1021	CGTCAGATCCGCTGGAGACGCCATCCAACGCTGTTTTGACCTCCATAGAGACACCGGGAC	1080	2092	CCGGCCACACTGTGTGGATTGTGTAGCTCTCTCGCACAGGCGCCACAGAGAGAGTCC	2151
DB	917	CGTCAGATCCGCTGGAGACGCCATCCAACGCTGTTTTGACCTCCATAGAGACACCGGGAC	976	1997	GCAGCGCCACCGAGGC-----TAGCAGCTTGAAGTGTGACCGGCTTGAAGAACGACA	2047
QY	1081	CGATCCAGCTCCGCGCGGGAAACGGTGCAATTTGGAACGCGGATTCCTCGTCCCAAGAGT	1140	2152	AGCTGATCAACACCAACCGCAGTTGGCACTCAATAGCAGCGGCCCTTGAACTGCAATGATA	2211
DB	977	CGATCCAGCTCCGCGCGGGAAACGGTGCAATTTGGAACGCGGATTCCTCGTCCCAAGAGT	1036	2048	CCAAACACCAACAGCAGCAGCGCGCGCATGATCATGGAGAGGGCGAGATCAAGAACTGCA	2107
QY	1141	GAGTAAAGTACCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCAATGCTATA	1200	2212	GCCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCAACCAAGTTCAACTCTTCAAGCT	2271
DB	1037	GAGTAAAGTACCGCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCAATGCTATA	1096	2108	GCTTCAACATCAGCATCCGCGGCAAGGTGCAAGAGGATACGCTTCTTCTTAC	2167
				2272	GTCTGAGAGGCTAGCCAGCTCCGACCCCTTACCGATTTTGACCAGGGCTGGGGCCCTA	2331

Db 2168 AGCTGGACATCATCCCATCGACAACACACACACACAGCTACAGCCTGACAGCTGCAACA 2227
Qy 2332 TCAGTTATGCAACGGAAGCGGCCCGACACAGCGCCCTACTGCTGGCACTACCCCCA - 2390
Db 2228 CCAGCGTATACCCAGCGCTGCCCAAGGTAGCTTCGAGCCCATCCCCAACCACTACT 2287
Qy 2391 --AAACCTTCGGGTATTGTGCCCGCGAAGAGTGTGTGTGTCGGGTATATTGTCTCACTC 2448
Db 2288 GCGCCCCCGCGCTTCGCCATCTGAAGTGAAGGACAAGAGTTCAACGGCAAGGGCC 2347
Qy 2449 CCAGCCCCGTGGT- ----GTGGNAACGACGACGAGTGGCGGGCGGCCCACTACAGCTGG 2504
Db 2348 CTTGCAACCAAGTGAAGCAGCTGAGTGCAGTGCACCAACGCGATCCGCGCCGCTGGAGCACCC 2407
Qy 2505 GGTGAAATGATACGAGCTTCCTGCTCTTAACAATACACAGGCCACCGCTGGGCAATTGG 2564
Db 2408 AGCTGCTGTAACGGTAGCTGGCCGAGGAGGAGTGTGTATCCGAGCGCTAACTTCG 2467
Qy 2565 TTCGGTTGTACCTGGATGAACCTCAACTGGATTCAACAAAGTGTGCGGAGCGCCT - -CCITT 2622
Db 2468 CCGACAAAGCAAGTGATCATCGTGCAGCTGAACGAGAGCGTGGAGATCAACTGCACCC 2527
Qy 2623 GTGTATCGAGGGCGGGCAACAAACCTGCACTGCCCACTGATTTGTTTCGCAAGC 2682
Db 2528 GCGCCAAACAACAACCGCAAGAGCATCCACATCGCGCCGCGCGCTTCTACACCA 2587
Qy 2683 ATCCGAGGCCACATATCTCGGTGGCGCTCGGTCCCTGGATCACACCCAGTGCCTGG 2742
Db 2588 CCGCGAGATCATCGGCGACATCGCGCAGGCCCACTGCAACCTGAGCGCGCCCAAGTGA 2647
Qy 2743 TCAGTACCCGTATAGCTTTGGCATTTATCTGTATACCACTCAACTACACCATATTTAAAA 2802
Db 2648 ACACACCTTGACAAAGATCGTGNATCAAGCTGCGGAGCAGTTGCGCAACAAGACCATCG 2707
Qy 2803 TCAGGATGTACGTGGAGGGTGAACACAGGTGGAAAGTGTGCTGCAACTGACGCGGG 2862
Db 2708 TGTTCAGCAACAGCGCGGGGACCCCGAGATCGTGACCCACAGCTTCAACGTGGCGG 2767
Qy 2863 GCGAAGTTCGGATCTGGAGATAGGACAGGTCCGAGATCGATATGAGAAATCATCAT 2922
Db 2768 GCGAGTTCTTCTACTGCAACAGCACCCAGCTGTGTTCAACAGCAGCCTGTGTTCAACAGCACCT 2827
Qy 2923 CAGGATTCCTAGGACCCCTGCTGTGTACAGCGGGGTTTTTCTTTGACAAAGATCC 2982
Db 2828 GGAGCACGAGGCAACAAC - - - - -ACCGAGGCGCAGCGACACCATCACCTGCGCT 2881
Qy 2983 TCACAATACCGCAGAGTCTAGACTCGTGGTGAATCTCTCAATTTTCTAGGGGATCTC 3042
Db 2882 GCGGCATCAAGCAGATCATCAACATGTGGCAAGGTGGGCAAGGCCATGTAGCGCCCC 2941
Qy 3043 CCGTGTCTTGGCCAAAATTCGAGTCCCAACCTCCAATCACTACCAACCTCTCTGTC 3102
Db 2942 CCATCAGCGCCAGATCCGCTGCAGCAGCAACATCAACCGCCCTGCTGCTGACCCGGAAG 3001
Qy 3103 CTCCAATTTGCTGTGTTATCGTGGATGTGTGCGGCGTTTTTATCATATTCTCTTCA 3162
Db 3002 GCGCAACACAAACGAGCGAGATCTTCGTCCGCGGGGGGACATGGCGACA 3061
Qy 3163 TCCTGTGCTATGCTCATCTTTATTTGTTTCTTCTGGAATTATC - - - - -AAGTATGTTG 3218
Db 3062 ACTGGCGCAGCAGCTGTACAAGTACAAGTGTGAAGATCGAGCCCTCGGCGTGGGCC 3121
Qy 3219 CCGTTTGTCTCTAATTCAGGATCAACAAACAGTACGGGACCATGCAAAACCTGTC 3278
Db 3122 CCACCAAGGCCAAGCTTACCGTCCAGGCCCGCAGCTGTGAGCGGCATCTGTCAGCAGC 3181
Qy 3279 ACAGCTCTGCTCAAGCAACTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACCGAT 3338
Db 3182 AGAACAACTGTGGCGGCATCGAGGCCGAGACCTGCTGACGTACCGTGTGGG 3241
Qy 3339 GGAATTTGCACTGTATTTCCCATCCCATCGTCTCTGG - - - - -GCTTTGCAAAATACCTATGG 3395

Db 3242 GCATCAAGCAGCTGCAAGCGCCGACCCCTGGCCGTGGAGCGCTACCTGAAGACACGACG 3301
Qy 3396 GAGTGGCGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCAATTTGTTTCACTGTTT 3455
Db 3302 AGCTCAGCAGATCTGGAACCAACACACCTGGAATGAGTGGGACCGGGAGATCAACAACT 3361
Qy 3456 GTAGGCGCTTCCCCCACTGTTTGGCTTTTCACTATATGATGATGATGATGATGATGATG 3515
Db 3362 ACACGAGCTGATCCACAGCTGATCGAGGAGAGCCAGAACACGACGAGAACAGCAGC 3421
Qy 3516 AGTCTGTACAGCATCGTGAAGTCCCTTTATACCGCTGTTACCAATTTTCTTGTCTCTGG 3575
Db 3422 AGAGCTGTGAGCTGGAAGTGGGCGAGCTGTGGAACCTGTTCAACATCACCAACT 3481
Qy 3576 GTATACATTTAAGAAATTCAGACTCGAGCAAGTCTAGAAAGCGCGCCCAAGATATCAAGGA 3635
Db 3482 GCGTGTGTACATCAAGCTGTTTCAATCATGATCGTGGCGGCTGTGGGCTCGGCATCG 3541
Qy 3636 TCCACTACGCG - TTAGAGCTCGCTGATCAGCTCGACTGCTGCTTCTAGTTGCGAGCCAT 3694
Db 3542 TGTTCGCGTGTGAGCATCTGAGGATCCAGATCTGCTGTGCTTCTAGTTGCGAGCCAT 3601
Qy 3695 CTGTTGTTGCGCTCCCGCTGCTTCTTGAACCTTGAAGTGCACCTCCCACTGCTCC 3754
Db 3602 CTGTTGTTGCGCTCCCGCTGCTTCTTGAACCTTGAAGTGCACCTCCCACTGCTCC 3661
Qy 3755 TTTCTTAATAAATGAGAAATTTGATCGATCGATTTGCTGAGTAGTGTGTCATTCTATTCTGG 3814
Db 3662 TTTCTTAATAAATGAGAAATTTGATCGATCGATTTGCTGAGTAGTGTGTCATTCTATTCTGG 3721
Qy 3815 GGGTGGGTGGGCGAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGGATGCTG 3874
Db 3722 GGGTGGGTGGGCGAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGGATGCTG 3781
Qy 3875 GGAGC - - - - - 3880
Db 3782 GGGATCGGTGGGCTCTATGGGTACCCAGTGTGTAAGAATTTGACCCGGTTCTCTCTGGG 3841
Qy 3881 - - - - - 3880
Db 3842 CCAGAAAGACGAGGACATCCCTTCTGTGTGACACACCTGTCCAGCCCTCGTTCT 3901
Qy 3881 - - - - - 3880
Db 3902 TAGTTCAGCCCACTCATAGGACACTCATAGCTCAGGAGGCTCCGCTTCAATCCAC 3961
Qy 3881 - - - - - 3880
Db 3962 CCGCTAAAGTACTTTGGAGGGTCTCTCTCTCTCATCAGCCCAACCAACCTAGC 4021
Qy 3881 - - - - - 3880
Db 4022 CTCGAAGGTGGGAAGAAATTAAGCAAGATAGGCTATTAAAGTGCAGAGGAGAGAAAT 4081
Qy 3881 - - - - - 3880
Db 4082 GCTCCCAACATGTGAGGAAGTAATGAGAAATCATAGAATTTTAAGGCCATCATGSCCT 4141
Qy 3881 - - - - -TCCTTCGCTTCTCGCTCACTGACTGCTGCGCTCGGTCTGCTTGGCTGGCGAGCG 3937
Db 4142 TAATCTTCGCTTCTCTCGCTCACTGACTCGCTCGCTCGGTCTGCTTGGCTGGCGAGCG 4201
Qy 3938 GTATCAGCTCACTCAAGGGGTAAATACGTTATCCAGAAATCAGGGGATACGAGGA 3997
Db 4202 GTATCAGCTCACTCAAGGGGTAAATACGTTATCCAGAAATCAGGGGATACGAGGA 4261
Qy 3998 AAGAAATGTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAAAGCGCGGTGCTG 4057
Db 4262 AAGAAATGTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAAAGCGCGGTGCTG 4321
Qy 4058 GCGTTTTTCATAGGCTCGCGCCCTGACAGCAGCATCAAAAATCGACGCTCAAGTCA 4117
Db 4322 GCGTTTTTCATAGGCTCGCGCCCTGACAGCAGCATCAAAAATCGACGCTCAAGTCA 4381

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QY 4118 AGTGGCGAAACCCGACAGACTATAAAGATACCAGGCGTTTCCCGCTGGAAGCTCCCTC 4177
Db 4382 AGTGGCGAAACCCGACAGACTATAAAGATACCAGGCGTTTCCCGCTGGAAGCTCCCTC 4441
QY 4178 GTGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTCG 4237
Db 4442 GTGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTCG 4501
QY 4238 GGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGTATCTCAGTTTCGGTGTAGTGTGTT 4297
Db 4502 GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTTCGGTGTAGTGTGTT 4561
QY 4298 CGTCCGAGTGGGCTGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCC 4357
Db 4562 CGTCCGAGTGGGCTGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCC 4621
QY 4358 GGTAACTATCGTCTGAGTCCAAACCCGCTAAGACACGACTTATCGCCACTGGCAGCAGCC 4417
Db 4622 GGTAACTATCGTCTGAGTCCAAACCCGCTAAGACACGACTTATCGCCACTGGCAGCAGCC 4681
QY 4418 ACTGTAACAGGATTAACGAGCGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGG 4477
Db 4682 ACTGTAACAGGATTAACGAGCGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGG 4741
QY 4478 TGGCCTAACTACGGCTACACTAGAAGACAGATATTTGGTATCTGCGCTCTGTGAAGCCA 4537
Db 4742 TGGCCTAACTACGGCTACACTAGAAGACAGATATTTGGTATCTGCGCTCTGTGAAGCCA 4801
QY 4538 GTTACCTTCGGAAGAGTTGCTAGCTCTTGATCCGGCAACACACCGCTGCTAGC 4597
Db 4802 GTTACCTTCGGAAGAGTTGCTAGCTCTTGATCCGGCAACACACCGCTGCTAGC 4861
QY 4598 GGTGGTTTTTTTCTTGAAGCAGACAGATTACGCGCAGAAAAAAGGATCTCAAGAGAT 4657
Db 4862 GGTGGTTTTTTTCTTGAAGCAGACAGATTACGCGCAGAAAAAAGGATCTCAAGAGAT 4921
QY 4658 CTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAAGAAACTCAGTTAAGGAT 4717
Db 4922 CTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAAGAAACTCAGTTAAGGAT 4981
QY 4718 TTGCTCATGAGATTATCAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAATCAAGT 4777
Db 4982 TTGCTCATGAGATTATCAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAATCAAGT 5041
QY 4778 TTTAAATCAATCTAAAGTATATAGTAAACTTGGTCTGACAGTTTACCAATGCTTAATC 4837
Db 5042 TTTAAATCAATCTAAAGTATATAGTAAACTTGGTCTGACAGTTTACCAATGCTTAATC 5101
QY 4838 AGTGAGCAGCTATCTCAGGATCTGTCTATTTGTTTCATCCATAGTTGCTGACTC 4894
Db 5102 AGTGAGCAGCTATCTCAGGATCTGTCTATTTGTTTCATCCATAGTTGCTGACTC 5158
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RESULT 11

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US-10-359-120-15
; Sequence 15, Application US/10359120
; Publication No. US20040033487A1
; GENERAL INFORMATION:
; APPLICANT: NABLE, Gary J.
; APPLICANT: CHAKRABARTI, Bimal K.
; APPLICANT: HUANG, Yue
; TITLE OF INVENTION: MODIFICATIONS OF HIV Env, Gag, AND Pol
; FILE OF INVENTION: ENHANCE IMMUNOGENICITY FOR GENETIC IMMUNIZATION
; FILE REFERENCE: NIH206.001C1
; CURRENT APPLICATION NUMBER: US/10/359,120
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: PCT/US01/25721
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/279,257
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/252,115
; PRIOR FILING DATE: 2000-11-14
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; PRIOR APPLICATION NUMBER: US 60/225,097
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6505
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid pVR1012x/s containing HIV genes
US-10-359-120-15
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Query Match 38.8%; Score 2283.4; DB 17; Length 6505;
Best Local Similarity 69.5%; Pred. No. 0;
Matches 3656; Conservative 0; Mismatches 1061; Indels 546; Gaps 19;

QY 1 TCGCGCGTTTCGGTGATGACCGTGAAACCTCTGACACATGAGCTCCCGGAGACGGTCA 60
Db 1 TCGCGCGTTTCGGTGATGACCGTGAAACCTCTGACACATGAGCTCCCGGAGACGGTCA 60
QY 61 CAGCTTGTCTGTAAGCGGATGCCGAGAGCAGACAAGCCCGTCAGGCGCGCTCAGCGGGTG 120
Db 61 CAGCTTGTCTGTAAGCGGATGCCGAGAGCAGACAAGCCCGTCAGGCGCGCTCAGCGGGTG 120
QY 121 TTGGCGGGTGTCCGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGC 180
Db 121 TTGGCGGGTGTCCGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGC 180
QY 181 ACCATATGAAGCTTTTTCGCAAAAGCTAGGCGCTCCAAAAAGCCTCCTCAGTCTTCGG 240
Db 181 ACCATATGGG-----TGTGAATACCGCACA 207
QY 241 AATAGCTCAGAGCGCGAGCGGCTCGGCTCTGTCATTAATAAAAAAATTAGTCAGCCA 300
Db 208 GATGCGTAAGGAAAAATACCGCATCAG-----235
QY 301 TGGGGCGGAGATGGCGGAACCTGGGCGGGAGGGAATTTATTGGCTATTGGCCATTGCA 360
Db 236 -----ATTGGCTATTGGCCATTGCA 256
QY 361 AGCTTGTATCTATATCAATAATGTACATTTATATTGGCTCATGTCCAATATGACGCCA 420
Db 257 AGCTTGTATCCATATCAATAATGTACATTTATATTGGCTCATGTCCAATATGACGCCA 316
QY 421 TGTGACATTGATTATGACTAGTTATTAAAGTAACTCAATTAACGGGTCATTAGTTCA 480
Db 317 TGTGACATTGATTATGACTAGTTATTAAAGTAACTCAATTAACGGGTCATTAGTTCA 376
QY 481 AGCCCATATGAGTTCGCGCTTACATAAATTCAGGTAATAATGGCCGCTGGCTGACCG 540
Db 377 AGCCCATATGAGTTCGCGCTTACATAAATTCAGGTAATAATGGCCGCTGGCTGACCG 436
QY 541 CCCAACGACCCCGCCCATTTGACGTCATTAATGAGTATGTTCCCATAGTAAGCCCAATA 600
Db 437 CCCAACGACCCCGCCCATTTGACGTCATTAATGAGTATGTTCCCATAGTAAGCCCAATA 496
QY 601 GGGACTTTCATGACGTCATTAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 660
Db 497 GGGACTTTCATGACGTCATTAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 556
QY 661 CATCAAGTGTATCATATGCAAGTCCGCGCTTATGAGTCAATGAGCGTAAATGGCCCG 720
Db 557 CATCAAGTGTATCATATGCAAGTCCGCGCTTATGAGTCAATGAGCGTAAATGGCCCG 616
QY 721 GCTGGCATTATGCCAGTACATGACCTTACGGGACTTTCTTCTTGGCAGTACATCTAC 780
Db 617 GCTGGCATTATGCCAGTACATGACCTTACGGGACTTTCTTCTTGGCAGTACATCTAC 676
QY 781 GTATTAGTCAATCGCTATTACCAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 840
Db 677 GTATTAGTCAATCGCTATTACCAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 736
QY 841 TAGCGTTTGAAGTCAAGGAGTTTCCAAAGTCTCCACCCCAATGACGTCATTAAGGAGTTG 900
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Db 737 |||||TAGCGGTTGACTCAGCGGGAATTCGAAGTCTCCACCCCAATTGACGTCATGCGAGTTTG 796
Qy 901 |||||TTTGGCACCACAAATCAACGGGACTTTTCCAAAATGTCGAATTAACCCCGCCCGTTGACG 960
Db 797 |||||TTTGGCACCACAAATCAACGGGACTTTTCCAAAATGTCGAATTAACCCCGCCCGTTGACG 856
Qy 961 |||||CAAATGGCGGTAGGCGTGTA CGGTGGGAGTCTATATAAGCAGAGTCTGTTTAGTGAAC 1020
Db 857 |||||CAAATGGCGGTAGGCGTGTA CGGTGGGAGTCTATATAAGCAGAGTCTGTTTAGTGAAC 916
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Qy 1380 |||||ATACTCTGCTTTCAGAGACTGACAGGACTCTGTATTTTTCAGAGATGGGGT-CCATTT 1438
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Db 1397 |||||CATAGCGTGGGATCTCCACGGAATCTCGGGTACGTGTTCCGGACATGGGCTCTCTCCG 1456
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Db 1517 |||||TCGGCAGCTCTGCTCCTTAACAGTCGGAGCCAGACTTATGGCAGACGACAAATGCCACCA 1576
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Db 1577 |||||CCACCAAGTGTCCGCGCAAGAGCCGCTGGCGTAGGGTATGTCTGAAAATAGCTCGGAG 1636
Qy 1736 |||||ATTGGGCTCGCAC-CTGGAGCGCAGATGGAAGACTTAAGGCGAGCGGCGAGAAGATGCGAG 1794
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Qy 1795 |||||GCAGCTGAGTGTGTATTTCTGATAGAGTCAGAGGTAACTCCGTTGGGTGCTGTTAA 1854
Db 1697 |||||GCAGCTGAGTGTGTATTTCTGATAGAGTCAGAGGTAACTCCGTTGGGTGCTGTTAA 1756
Qy 1855 |||||CGGTGAGGCGCAGTGTAGTCTGAGCAGTACTCTGCTGCGCGCGCGCCACAGACATA 1914
Db 1757 |||||CGGTGAGGCGCAGTGTAGTCTGAGCAGTACTCTGCTGCGCGCGCGCCACAGACATA 1816
Qy 1915 |||||ATAGCTGACAGACTAAACAGACTGTTCTTTTCCATGGGTCTTTTCTGCAGTCAACCGTCGTC 1974

Db 1817 |||||ATAGCTGACAGACTAAACAGACTGTTCTTTTCCATGGGTCTTTTCTGCAGTCAACCGTCGTC 1876
Qy 1975 |||||GACGAATTCAGACA---ATCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTCGCTGTC 2031
Db 1877 |||||GACACGTGTGATCAGATATCGCGCCGCTCTTAGACACCATGCGGTGAAGGAGATACC 1936
Qy 2032 |||||TGTTGGAGCAGTCTTTCGTTTTCGCGCAGCGCTAGCGAAAACCCACGTCAACCGGGGAGTG 2091
Db 1937 |||||AGCACCTGTGGCGCTGGGCTGCGCTGGGCGACCATGCTGCTGGGCATGCTGATGATCT 1996
Qy 2092 |||||CCGGCCACACTGTCTGTGATTTTGTAGGCTCTCTCCACAGCGCGCAGCAGCAACGTCC 2151
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Qy 2212 |||||GGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTTCAACTCTTCAGGCT 2271
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Qy 2392 |||||AACCTTTCGGTATTTGTCGCCGGAAGAGTGTGTGTGCGGTATATTTGCTTCACTCCCA 2451
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Db 2687 |||||AGTTCCGCAA---CAAAGCACTCGTGTTCAAAGCACAGCAGCGCGCGCGCCGAGATC 2742
Qy 2872 |||||GCGATCTGGAAGTAGGAGCAGTCCGAGATCGATATGGAGAACATCAACATCAGGATTC 2931
Db 2743 |||||GTGACCCACAGCTTCAACTGCGCGCGGAGTTCTTCTACTGCAACAGACCCAGCTGTTTC 2802
Qy 2932 |||||TAGGACCCCTGCTGCTGTGTACAGGGCGGGTTTTTCTTGTGTGACAAGATCTCTCAATAC 2991
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Qy 2992 |||||CCGAGAGTCTAGCTGCTGGTGAATTTCTCTCAATTTTCTAGGGGATCTTCCCGTGTGTC 3051
Db 2863 |||||GACACCATCACCTGCGCTGCGCATCAAGCAGATCATCAACATGTGGCAGAGAGTGGC 2922

QY	3052	TTGGCCAAAATTGCGAGTCCCCAACTCCATCATCTACCAACCTCCTGTCTCCAAATTT	3111	QY	3879	-----	3878
DB	2923	AAAG-----CCATGTACGCCCCCCCATCATCGCGGCAGATCC	2959	DB	3964	AGAAATTAAAGCAAGATAGGCTATTAAAGTGCAGAGGAGAGAAATGCTTCCAAATGTG	4023
QY	3112	GTCCCTGGTTATCGCTGGATGTGTCGGGGTTTTATCATATTCCCTTTCATCCTGCTGC	3171	QY	3879	-----GCTCTTCCGCTTC	3891
DB	2960	GCTGCAGCAGCAACATCACCGGCTCTGCTGACCCCGCAGCGGCAACAGCAACAACG	3019	DB	4024	AGGAAGTAATGAGAGAAATCATAGAAATTTTAAGGCCATCATGGCCTTATCTTCCGCTTC	4083
QY	3172	TATGCTCATCTTTCTTAATTGTTTCTTGGAATTTCAAGGTATGTTGC-CCGTTGTCTCT	3230	QY	3892	CTCGCTCACTGACTCGCTCGCTCGGTCTCGGTCTGGCTGGCGCAGCGGTATCAGCTCACTC	3951
DB	3020	AGAGCGAGATCTTCCTCGCGGGCGGCGACATGCGCGACAACCTGCGCAGCGAGCTGT	3079	DB	4084	CTCGCTCACTGACTCGCTCGCTCGGTCTCGGTCTGGCTGGCGCAGCGGTATCAGCTCACTC	4143
QY	3231	CTAAATTCAGGATCAAACAACAACGATACGGGACCAATGCAAAACCTGCAACGATCTCTGT	3290	QY	3952	AAAGGGGTAAATACGGTTATCCACAGATCAGGGGATACCGCAGGAAAGAAATGTGAGC	4011
DB	3080	ACAAATACAAAGTGTGAAGATCGAGCC-----CTGGCGCTGGCCCCCAACCAAGG	3130	DB	4144	AAAGCGGTAAATACGGTTATCCACAGATCAGGGGATACCGCAGGAAAGAAATGTGAGC	4203
QY	3291	CAAGGCAACTATGTTTCCCTCATGTTCTGTACAAACCTACGGATGGAATTGCACC	3350	QY	4012	AAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGCGCGGTTGCTGGCGGTTTTTCCATAG	4071
DB	3131	CAAGCTTAACGTTCCAGGCCCGGACGCTGCTGAGCGGCATCGTGCAGCAGCAACAAC	3190	DB	4204	AAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGCGCGGTTGCTGGCGTTTTTCCATAG	4263
QY	3351	TGTATTCCCATCCCATCTGCTGGGCTTTGCAAAAATACCTATGGGAGTGGGCTCAGTC	3410	QY	4072	GCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAAGAGTGGGAAACCC	4131
DB	3191	TGCTGCGCCATCGAGGCCAGCAGCACTGCTGCAGCTGACCGTGTGGGGCATCAAGC	3250	DB	4264	GCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAAGAGTGGGAAACCC	4323
QY	3411	CGTTTCTCTTGGCTCAGTTTATAGTGGCAATTTGTTCACTGGTTCTGATGGGCTTTCCCCC	3470	QY	4132	GACAGACTATAAAGATACCAAGCGGTTTTCCCTCGAAGCTCCCTCGTGGCTCTCCTGT	4191
DB	3251	AGCTGCAGGCC-CGCAACCTGGCGGTGGAGCGGTACTCTGAAGGACGAGCAGCTCGAG	3309	DB	4324	GACAGACTATAAAGATACCAAGCGGTTTTCCCTCGAAGCTCCCTCGTGGCTCTCCTGT	4383
QY	3471	ACTGTTTGGCTTTCAGCTATATGATGATGTGTATTTGGGGCCAACTGTGTACAGCATC	3530	QY	4192	TCCGACCTTCCGCTTACCGGATACCTGTCCGCCCTTTCTCCCTTGGGAAGGCTGGCGCT	4251
DB	3310	CAGATCTGGAAACACACCACTGGATGGAGTGGACCGCGAGATCAACAATACACGAC	3369	DB	4384	TCCGACCTTCCGCTTACCGGATACCTGTCCGCCCTTTCTCCCTTGGGAAGGCTGGCGCT	4443
QY	3531	GTGAGTCCCTTTATACCGCTGTGTACCAATTTTCTTTGTCTCTGGGTATACATTTAAGAA	3590	QY	4252	TTCTCAATGCTCACGCTGTAGGTATCTCAGTTTGGGTAGGTGCTTCCCTCAAGCTGGG	4311
DB	3370	CTGATCCAC-----AGCCTGATCGAGAGAGCCAGAACCGACGAGAGAAGCAGCAG	3423	DB	4444	TTCTCATAGCTCACGCTGTAGGTATCTCAGTTTGGGTAGGTGCTTCCCTCAAGCTGGG	4503
QY	3591	TTCAGACTCGAGCACTAGAAAGCGCGCCAGATATCAAGGATCCACTACGCGTTAG	3650	QY	4312	CTGTGTGACGAAACCCCGGTTACGCCGACCGCTCGCGCTTATCCGGTAACTATCGTCT	4371
DB	3424	GAGCTCTGGAGTGACAAAGTGGGCGAGCTGTGGAACTGTGTTCAACATCAACCACTGG	3483	DB	4504	CTGTGTGACGAAACCCCGGTTACGCCGACCGCTCGCGCTTATCCGGTAACTATCGTCT	4563
QY	3651	AGCT--CGCTGATCAGCTCGACTGCTCTAGTTGCGAGCACTCTGTGTTGGCCCC	3708	QY	4372	TGAGTCCAAACCCGGTAAAGACACGACTTATCGCCACTTGGCAGCAGCCACTTGGTAAACAGGAT	4431
DB	3484	CTGTGTGAGGATCCAGATCTGCTGTGCTCTTCTAGTTTGCAGGCATCTGTGTTGCCCC	3543	DB	4564	TGAGTCCAAACCCGGTAAAGACACGACTTATCGCCACTTGGCAGCAGCCACTTGGTAAACAGGAT	4623
QY	3709	TCCCCCGTCCCTTCTTGACCCCTGGAAAGTGGCACTCCCACTGCTCTTCTTAATAAAAT	3768	QY	4432	TAGCAGAGCGAGTATGATGAGCGGTCTACAGATTTCTTGAAGTGGTGGCTTAACTACGG	4491
DB	3544	TCCCCCGTCCCTTCTTGACCCCTGGAAAGTGGCACTCCCACTGCTCTTCTTAATAAAAT	3603	DB	4624	TAGCAGAGCGAGTATGATGAGCGGTCTACAGATTTCTTGAAGTGGTGGCTTAACTACGG	4683
QY	3769	GAGGAAATTGCATCGCATTTGTCTGAGTAGGTGTCTATTCTATTCTGGGGGTGGGGTGGG	3828	QY	4492	CTACACTAGAGGACAGATTTTGGTATCTGCGCTCTGCTGAAAGCCAGTTTACCTTCGAAA	4551
DB	3604	GAGGAAATTGCATCGCATTTGTCTGAGTAGGTGTCTATTCTATTCTGGGGGTGGGGTGGG	3663	DB	4684	CTACACTAGAGGACAGATTTTGGTATCTGCGCTCTGCTGAAAGCCAGTTTACCTTCGAAA	4743
QY	3829	CAGGACAGAGGGGAGGATTTGGGAAGACAATAGCAGGCATGCTGGGATCGGGTGGG	3878	QY	4552	AAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGTGTAGCGGTGGTTTTTGT	4611
DB	3664	CAGGACAGAGGGGAGGATTTGGGAAGACAATAGCAGGCATGCTGGGATCGGGTGGG	3723	DB	4744	AAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGTGTAGCGGTGGTTTTTGT	4803
QY	3879	-----	3878	QY	4612	TTGCAAGCAGCAGATTAACCGCAGAAAAAAGGATCTCAAGAGATCTCTTTGATCTTTTC	4671
DB	3724	TCTATGGGTACCCAGGTGCTGAAGATTGACCCGGTTCTCTCTGGGCCAGAAAGACAG	3783	DB	4804	TTGCAAGCAGCAGATTAACCGCAGAAAAAAGGATCTCAAGAGATCTCTTTGATCTTTTC	4863
QY	3879	-----	3878	QY	4672	TACGGGTTGACGCTCAGTGAAGCAAACTCAGCTTAAAGGATTTTTCGTCATGAGATT	4731
DB	3784	GCACATCCCTTCTCTGTGACACACCTCTGTCCACGCCCCCTGTTCTTAGTTCCAGCCCCA	3843	DB	4864	TACGGGTTGACGCTCAGTGAAGCAAACTCAGCTTAAAGGATTTTTCGTCATGAGATT	4923
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DB	3844	CTCATAGGACACTCATAGCTCAGGAGGGCTCGCCCTTCAATCCACCCCGTAAAGTACTTT	3903	DB	4924	ATCAAAAAAGGATCTTTCACCTAGATCTTTTAAATTAATAAAGTAAAGTTTAAATCAATCTA	4983
QY	3879	-----	3878	QY	4792	AAATATATATAGTAAAACTTTGGTCTGACAGTTTAACTAGTGAAGTAACTAGTGAAGTAACT	4851
DB	3904	GGAGCGGTCTCTCCCTCCCTCATCGCCCAACCAACCAACCTAGCCTCCAAAGAGTGGGA	3963	DB	4984	AAATATATATAGTAAAACTTTGGTCTGACAGTTTAACTAGTGAAGTAACTAGTGAAGTAACT	5043
				QY	4852	CTCAGCGATCTGTCTATTCTTTCGTTTCATCCATAGTTGCTGACTC	4894

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Db 5044 CTCAGCGATGTCGTCATTTGCTTCATCCATAGTTCGCTGACTC 5086
|||||
RESULT 12
US-10-359-120-34
; Sequence 34, Application US/10359120
; Publication No. US20040033487A1
; GENERAL INFORMATION:
; APPLICANT: NABLE, Gary J.
; APPLICANT: CHAKRABARTI, Bimal K.
; APPLICANT: HUANG, Yue
; TITLE OF INVENTION: MODIFICATIONS OF HIV Env, Gag, AND Pol
; FILE OF INVENTION: ENHANCE IMMUNOGENICITY FOR GENETIC IMMUNIZATION
; FILE REFERENCE: NIH206.001C1
; CURRENT APPLICATION NUMBER: US/10/359,120
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: PCT/US01/25721
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/279,257
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/252,115
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/225,097
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 6460
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid pVr1012x/s containing HIV genes
US-10-359-120-34

Query Match 38.8%; Score 2283; DB 17; Length 6460;
Best Local Similarity 69.9%; Pred. No. 0;
Matches 3595; Conservative 0; Mismatches 1195; Indels 355; Gaps 24;

QY 1 TCSCGGTTCGCTGATGAGCGTGAAACCTCTGACACATGACGCTCCCGAGACGGTCA 60
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QY 481 AGCCCATATATGAGTTTCGCGTTACATAACTTACGGTAAATGGCCGCTGGCTGACCG 540
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1736 ATTGGGCTCGCAC - CTGGACGCGAGATGGAGACTTAAGGCGAGCGGCGAGGAAGATGCGAG 1794
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3377 GCTGGACAGTGGCGCAGCTGTGGAACTGGTTCAACATCAACAACCTGCTGTGGTAGG 3436
3320 CTGTACAAAACCTACGATGGAAATTC---ACCTGATTTCCCATCCCATCTCTCTGGGC 3376
3437 ATCCAGATCTGCTGTGCTCTTAGTTGCGAGCATCTGTTTGGCCCTCCCTCCCGTGC 3496
3377 TTTTCGCAAAATACCTATGGGAGTGGGCTCAGTCCGTTCT-CTTGGCTCAGTTTACTAG 3435
3497 TTTCTTGACCTTGAAGGTGCCACTCCCACTGTCTTCTTAATAAATGAGGAATTCG 3556
3436 TGCCATTTGTTTCAGTGGTTCTGAGGGCTTTCCCACTGTTTTGGCTTTTTCAGCTATATGA 3495
3557 ATCGCATTTCTGCTGAGTAGTGTCTATTCTTGGGGGTGGGTGGGCGGACGACGAA 3616
3496 TGATGTGATTTGGGGGCAAGTCTGTACAGCATGCTGTAGTCCCTTTATACCGCTGTAC 3555
3617 GGGGAGGATTTGGGAAGACAATAGCAGGCATGCTGGGATGCGGTGGGCTCTATGGGTAC 3676
3556 CAATTTTCT-----TTTGTCTCTGGGTATACATTTTAAGAAITTCAGACTC--- 3599

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Db 3677 CCAGGTGCTGAGAAATGACCCGGTTCCTCTGGGCGAGAAAGCAGGCACATCCCT 3736
QY 3600 ---GAGCAAGTCTAGAAAGCGCGCCAGAGATATCAAGATCCACTACGGTTAGAGCTG 3656
Db 3737 TCTCTGTGACACACCTGTCTCAGCCCGCTGGTTCTTAGTTCCAGCCCACTCATAGACA 3796
QY 3657 CTGATCAGCCTCGACTGTGCTTCTAGTTGCGCAGCCATCTGTGTTGGCCCTCCGCCGT 3716
Db 3797 CTCATAGCTCAGGAGGGCTCCGCTTCAATCCACCGCTAAAGTACTTTGGAGGGGTCTC 3856
QY 3717 GCCTTCCTTGA-----CCCTGGAAGGTGCCATCTCCCATCTGCTCTTCTTAATAAATGA 3770
Db 3857 TCCCTCCCTCATCAGGCCCAACCAACCAACCTAGCCCTCCAGAGTGGGAAGAAATTAAG 3916
QY 3771 GGAATTTGCATCGCATTTGCTGAGTAGTGTCTATTTCTTCTGGGGGGTGGGGCGCA 3830
Db 3917 CAAGATAGGCTATTAAGTCAGAGGAGGAGAAATGCTCCAAATGTGAGGAAGTAATG 3976
QY 3831 GGACAGCAAGGGGAGGATTTGGGAAGACAAATAGCAGGCATGCTGG-GGAGCTCTCCGCT 3889
Db 3977 AGAGAAATCATAGAAATTTTAAGGCCATGATTTAAGGCCATCATGGCTTAATCTTCGCT 4036
QY 3890 TCTCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3949
Db 4037 TCTCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4096
QY 3950 TCAAGCGCGTATACGTTATCCACAGATCAGGGGATTAACCCAGGAAGACATGTGA 4009
Db 4097 TCAAGCGCGTATACGTTATCCACAGATCAGGGGATTAACCCAGGAAGACATGTGA 4156
QY 4010 GCAAAAGCGGCAGCAAAAGGCCAGAACCGTAAAGGCCGCTGCTGGGTTTTCCAT 4069
Db 4157 GCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAGGCCGCTGCTGGGTTTTCCAT 4216
QY 4070 AGGCTCGGCCCTCTGACGAGCATCAAAATTCGACGCTCAAGTCAGAGGTGGGAAAC 4129
Db 4217 AGGCTCGGCCCTCTGACGAGCATCAAAATTCGACGCTCAAGTCAGAGGTGGGAAAC 4276
QY 4130 CCGACAGGACTATAAGATACAGGGGTTTTCCCTGGAGCTCCCTCGTGGCTCTCCT 4189
Db 4277 CCGACAGGACTATAAGATACAGGGGTTTTCCCTGGAGCTCCCTCGTGGCTCTCCT 4336
QY 4190 GTTCCGACCTGCGCTTACCGGATACCTGTCTCGCCCTTTCTCCCTTCGGGAAGCTGGCG 4249
Db 4337 GTTCCGACCTGCGCTTACCGGATACCTGTCTCGCCCTTTCTCCCTTCGGGAAGCTGGCG 4396
QY 4250 CTTTCTCAATGCTCAAGCTGTAGGTATCTCAGTTTCGGGTGAGTGTGCTTCCCTCAAGCTG 4309
Db 4397 CTTTCTCATAGCTCAGGCTGAGGTATCTCAGTTTCGGGTGAGTGTGCTTCCCTCAAGCTG 4456
QY 4310 GGCTGTGTCAGCAACCCCGCTTACCGGACCGCTGCGCTTATCCGCTAATCTATCGT 4369
Db 4457 GGCTGTGTCAGCAACCCCGCTTACCGGACCGCTGCGCTTATCCGCTAATCTATCGT 4516
QY 4370 CTTGAGTCCAAACCGGTAGACACGACTTATCCCACTGGCAGCAGCACTGGTAACAGG 4429
Db 4517 CTTGAGTCCAAACCGGTAGACACGACTTATCCCACTGGCAGCAGCACTGGTAACAGG 4576
QY 4430 ATTAGCAGAGCGAGGTATGAGCGGTGTACAGATTTCTGAAGTGGTGGCTTAACCTAC 4489
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QY 4490 GGCTACACTAGAGGACAGTATTTGTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4549
Db 4637 GGCTACACTAGAGGACAGTATTTGTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4696
QY 4550 AAAAGAGTTGGTAGCTCTTCTGATCCGGCAAAACCAACCAACCGCTGCTGAGCGGTGTTTTT 4609
Db 4697 AAAAGAGTTGGTAGCTCTTCTGATCCGGCAAAACCAACCAACCGCTGCTGAGCGGTGTTTTT 4756
QY 4610 GTTTGCAAGCAGCAGATTACCGCCAGAAAGGATCTCAAGAGATCTTTGATCTTT 4669
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Db 4757 GTTTGCAAGCAGCAGATTACCGCCAGAAAAAAGGATCTCAAGAGATCTTTGATCTTT 4816
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Db 4817 TCTACGGGTCTGAGGCTCAGTGGAAAGAAACTCAGTTTAAGGATTTTGGTCATGAGA 4876
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RESULT 13
US-10-359-120-51
; Sequence 51, Application US/10359120
; Publication No. US20040033487A1
; GENERAL INFORMATION:
; APPLICANT: NABLE, Gary J.
; APPLICANT: CHAKRABARTI, Bimal K.
; APPLICANT: HUANG, Yue
; TITLE OF INVENTION: MODIFICATIONS OF HIV Env, Gag, AND Pol
; TITLE OF INVENTION: ENHANCE IMMUNOGENICITY FOR GENETIC IMMUNIZATION
; FILE REFERENCE: NIH206.001C1
; CURRENT APPLICATION NUMBER: US/10/359,120
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: PCT/US01/25721
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/279,257
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/252,115
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/225,097
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6577
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid pVR1012x/s containing HIV genes
US-10-359-120-51

Query Match 38.8%; Score 2280.4; DB 17; Length 6577;
Best Local Similarity 68.8%; Pred. No. 0;
Matches 3627; Conservative 0; Mismatches 1151; Indels 496; Gaps 16;

QY 1 TCAGCGGTTTCGGTGTATGACGGTGAACCTCTGACACATGACAGTCCCGGAGACGGTCA 60
Db 1 TCAGCGGTTTCGGTGTATGACGGTGAACCTCTGACACATGACAGTCCCGGAGACGGTCA 60
QY 61 CAGCTTGTCTGTAAAGCGGATGCCGGAGCAGACAAGCCCGTCAGGCGGCTCAGCGGGTG 120
Db 61 CAGCTTGTCTGTAAAGCGGATGCCGGAGCAGACAAGCCCGTCAGGCGGCTCAGCGGGTG 120
QY 121 TTGGCGGGTGTCCGGGCTGGCTTAACATATCGGCATCAGAGCAGATTGTACTCAGAGTGC 180
Db 121 TTGGCGGGTGTCCGGGCTGGCTTAACATATCGGCATCAGAGCAGATTGTACTCAGAGTGC 180
QY 181 ACCATATGAAGCTTTTTCGAAAGCCCTAGGCTCCAAAAAGCCCTCTCACTACTTCTGG 240
Db 181 ACCATATGCG-----TGTGAATATCCGCACA 207
QY 241 AATAGCTCAGAGCGCAGCGGCTCGGCTCTGCTGATAATAAAAAAATTAGTCAGCCA 300
Db 208 GATGCGTAAGGAGAAATATCCGCATCAG----- 235
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QY 301 TGGGCGGAGNATGGGGGNACTGGGCGGAGGGAATTAATGGCTATTGGCCATTGGCAT 360
Db 236 -----ATTGGCTATTGGCCATTGGCAT 256
QY 361 ACCTTGATCTATCATATAATATGATATATATTTGGCTCATGTCCAAATATGACGCCA 420
Db 257 ACCTTGATCCATATCATATATATGATATATTTGGCTCATGTCCAAATATGACGCCA 316
QY 421 TGTGACATTGATTAATGACTAGTTAATAGTAATCAATTAACGGGGTCATTAGTTTCAAT 480
Db 317 TGTGACATTGATTAATGACTAGTTAATAGTAATCAATTAACGGGGTCATTAGTTTCAAT 376
QY 481 AGCCCATATATGAGATTCCGGCTTACATAAATTACGGTAAATGGCCCGCTGGCTGACCG 540
Db 377 AGCCCATATATGAGATTCCGGCTTACATAAATTACGGTAAATGGCCCGCTGGCTGACCG 436
QY 541 CCCAAGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAAGCGCCAATA 600
Db 437 CCCAAGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAAGCGCCAATA 496
QY 601 GGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTTGGCAGTA 660
Db 497 GGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTTGGCAGTA 556
QY 661 CATCAAGTATCATATGCAAGTCCGCCCTTATTTGACGTCAATGACGGTAAATGGCCC 720
Db 557 CATCAAGTATCATATGCAAGTCCGCCCTTATTTGACGTCAATGACGGTAAATGGCCC 616
QY 721 GCCTGGCATATGCCAGTACATGACTTACGGGACTTTCCCTACTTTGGCAGTACATCTAC 780
Db 617 GCCTGGCATATGCCAGTACATGACTTATGGGACTTTCCCTACTTTGGCAGTACATCTAC 676
QY 781 GTATTAGTCAATGCTATTACATGATGCGTATGCGTTTGGCAGTACACCAATGGCGTGA 840
Db 677 GTATTAGTCAATGCTATTACATGATGCGTATGCGTATGCGTATGCGTATGCGTATGCG 736
QY 841 TAGCGTTTGGACTCAAGGGATTTCCAGTCTCCACCCCATTTGACGTCAATGGGAGTTTG 900
Db 737 TAGCGTTTGGACTCAAGGGATTTCCAGTCTCCACCCCATTTGACGTCAATGGGAGTTTG 796
QY 901 TTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCCGTTGACG 960
Db 797 TTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCGCCGTTGACG 856
QY 961 CAAAATGGGCGGTAGCGGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTATGTGAAC 1020
Db 857 CAAAATGGGCGGTAGCGGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTATGTGAAC 916
QY 1021 CGTCAGATCGCTGGAGAGCCCATCCACGCTGTTTGGACCTCCATAGAAGACACCGGGAC 1080
Db 917 CGTCAGATCGCTGGAGAGCCCATCCACGCTGTTTGGACCTCCATAGAAGACACCGGGAC 976
QY 1081 CGATCCAGCTCCGCGCGGGAAACGGTGTATGGAAACGGGATTCCTCGTGCAGAGT 1140
Db 977 CGATCCAGCTCCGCGCGGGAAACGGTGTATGGAAACGGGATTCCTCGTGCAGAGT 1036
QY 1141 GACGTAAGTACCGCTATAGCTCTATAGGCACACCCCTTTGGCTCTTATGCAATGCTATA 1200
Db 1037 GACGTAAGTACCGCTATAGCTCTATAGGCACACCCCTTTGGCTCTTATGCAATGCTATA 1096
QY 1201 CTGTTTTTGGCTGGGGCTATACACCCCGGCTTCCCTTATAGCTATAGGTATGTTATAGC 1259
Db 1097 CTGTTTTTGGCTGGGGCTATACACCCCGGCTTCCCTTATAGCTATAGGTATGTTATAGC 1156
QY 1260 TTAGCCTATAGGTGGGTATTGACATTAATGACACTTCCCTTATGGTGAAGTACT 1319
Db 1157 TTAGCCTATAGGTGGGTATTGACATTAATGACACTTCCCTTATGGTGAAGTACT 1216
QY 1320 TTCCATTACTAATCCATAACATGGCTCTTTGGCACAACCTATCTATTTGGCTATATGCCA 1379
Db 1217 TTCCATTACTAATCCATAACATGGCTCTTTGGCACAACCTATCTATTTGGCTATATGCCA 1276

QY 1380 ATACTGTGCTCTTTCAGAGACTGACCGGACTCTGTATTTTTCAGGATGGGT -CCATTT 1438
Db 1277 ATACTGTGCTCTTTCAGAGACTGACCGGACTCTGTATTTTTCAGGATGGGTGCCATTT 1336
QY 1439 ATTATTTACAAATTCACATATACAAACCGCGTCCCGGTGCCCGAGTTTTTATATAA 1498
Db 1337 ATTATTTACAAATTCACATATACAAACCGCGTCCCGGTGCCCGAGTTTTTATATAA 1396
QY 1499 CATAGCGTGGGATCTCC---GACATCTCGGGTACGTTTCCGGACATGGGCTCTTCTCCG 1555
Db 1397 CATAGCGTGGGATCTCCACCGGAATCTCGGGTACGTTTCCGGACATGGGCTCTTCTCCG 1456
QY 1556 GTAGCGCGGAGCTTCCACATCCGAGCCTGTGTCATCCGTCACGCGCTCATGTGCG 1615
Db 1457 GTAGCGCGGAGCTTCCACATCCGAGCCTGTGTCATCCGTCACGCGCTCATGTGCG 1516
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Db 1517 TCGGAGCTCTCTTGTCTTAAAGTGGAGGCGCAGACTTAGGCACACACAAATGCCACCA 1576
QY 1676 CCAACAGTGTCCGCAACAGCGCGTGGAGGTATGTCTGAAATAGACTCGGAG 1735
Db 1577 CCAACAGTGTCCGCAACAGCGCGTGGAGGTATGTCTGAAATAGACTCGGAG 1636
QY 1736 ATTGGGCTCGCACCTG-GACGAGATGGAAGACTTAAGCAGCGGCGCAGAGAGATGAG 1794
Db 1637 ATTGGGCTCGCACCTGAGCAGATGGAAGACTTAAGCAGCGGCGCAGAGAGATGAG 1696
QY 1795 GCAGCTGAGTGTGTATTTCTGATAAGACTCAGAGTAACTCCCGTTGCGGTCTGTAA 1854
Db 1697 GCAGCTGAGTGTGTATTTCTGATAAGACTCAGAGTAACTCCCGTTGCGGTCTGTAA 1756
QY 1855 CGGTGAGGCGAGTGTAGTCTGAGCAGTACTCGTTGCTCGCGGCGCGCCACACAGACATA 1914
Db 1757 CGGTGAGGCGAGTGTAGTCTGAGCAGTACTCGTTGCTCGCGGCGCGCCACACAGACATA 1816
QY 1915 ATAGCTGACAGACTAACAGACTGTTCTTTCATAGGCTCTTTTCTGACGTACCGCTC 1974
Db 1817 ATAGCTGACAGACTAACAGACTGTTCTTTCATAGGCTCTTTTCTGACGTACCGCTC 1876
QY 1975 GACGAATTCAGCA---ATCATGGATGCAATGAAGAGGGCTCTGCTGTGCTGCTGC 2031
Db 1877 GACAGCTGTGATCAGATATCGCGCGCTCTAGACACCATGCGGTGAAGAGAGTACC 1936
QY 2032 TGTGTGGAGCAGTCTTTCGTTTCGCGAGCGCTAGCGAAACCCACGTCACCGGGGAGTG 2091
Db 1937 AGCACCTGTGGCGCTGGGCTGCGCTGGGGACCATGTGCTGGGCATGCTGATGATCT 1996
QY 2092 CCGGCCACACTGTGCTGGATTGTTAGCTCTCTCGCACCCAGCGCCACAGCAACGTCC 2151
Db 1997 GCAGCGCCACCGAGAGAGTGTGGGTGACCGTGTACTACGGCGTGCCTGTGGAAGAGG 2056
QY 2152 AGCTGATCAACACCAACCGCAGTTGGCAGCTCAATAGACACGG---CCCTGAATGCAATG 2208
Db 2057 CCACCACCACTCTGCTCTCGCGCAGCGCACAGSCCTACGACACCGAGGTGCAACAG 2116
QY 2209 ATAGCCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCAGCAAGAGTTCAACTTTCAG 2268
Db 2117 TGTGGGCCACCCACGCTGCTGCGCCACCGACCCCAACCCCGAGGAGTGTGCTGGA 2176
QY 2269 GCTGTCTCAGAGGCTAGCCAGCTCGGACCCCTTACCGATTGACACAGGGCTGGGGC 2328
Db 2177 AGTGACCCAGAACTTTCGACATGTGGAAGAAAGCATGTGTGGAGCAGATGACAGAGACA 2236
QY 2329 CTATAGTTATGCCAACGGAAGCGGCCGACCGAGCGCCCTACTGCTGGCACTACCCCC 2388
Db 2237 TCATCA----GCCTGTGGGACAGAGCTGAAGCCCTCGGTGAAGCTGACCCCTGTG 2291
QY 2389 CAAAACCTTGGCGTATTTGCGCGGAGAGTGTGTGGTCCGGTATATTGTTCTCACTC 2448
Db 2292 CGTGAGCTGAGTGCACCGACC-TGAAGAACGACACCAACACCAACAGCAGCGGGC 2350
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Db 2351 GCATGATCATGGAGAGGGCGAGATCAAGAACTGACGCTTCAACATCAGCACCGCATCC 2410
Qy 2506 GTGAAAATGATAGCGAGCTCTCGTCTCTTAACTAACACCGCCACCGCTGGGCAATTGGT 2565
Db 2411 GCGCAAGGTGCAAGAGATGAGCTCTTCTTCAAGCTGGACATCATCCCATGACA 2470
Qy 2566 TCGGTGTATCTGATGAATCAACTGGAATTCACAAAGTGTGCGAGCGCCTCTTGTG 2625
Db 2471 ACGACACCAACAGCTACAGCTGACAGCTGCAACACCGCTAGCATCAATGCAACCGCC 2530
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Qy 2806 GATGTAGTGGAGGGGTGAAACACAGGCTGGAAGCTGCTGCAACTGGAACCGGGGCG 2865
Db 2711 TCAAGCACAGACGGCGGCGGCCCGGAGATCGTGACCCACAGCTTCAACTGCGGGCGG 2770
Qy 2866 AACGTTGCGATCTGGAGATAGGACAGGTCGAGATCGATATGGAGACATCACATCAG 2925
Db 2771 AGTTCTTCTACTGCAACAGACCCAGCTGTTCACAGACACCTGGTTCAACAGACCTGGA 2830
Qy 2926 GATTCTTAGGACCCCTGCTGCTGTATACAGCGGGTTTTTCTTTGTGACAAAGAACTCTCA 2985
Db 2831 GCACCGAGGGCAGCAAC- - - - - ACCGAGGCGAGCGACCACTACCCCTGCCCTGCC 2884
Qy 2986 CAATACCGCAGAGCTAGACTGTGGTGGATTCTCTCAATTTCTAGGGGATCTCCCG 3045
Db 2885 GCATCAAGCAGATCATCAACATGTGGCAGAGGTGGGCAAGGCCATGTACGCCCCGCCA 2944
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Db 3065 GCGCGAGCGAGCTGTACAAGTACAAGTGTGGAAGATCGAGCCCTTGGGCGTGGCCCCA 3124
Qy 3222 GTTTGCTCTAATTCAGAGATCAACAAACAGTACGGGACCATGCAAAACCTGCAG 3281
Db 3125 CCAAGGCCAAGCTTACCGTCCAGCGCGCCGAGCTGTGAGCGGCATCGTGACGACGAGA 3184
Qy 3282 ACTCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGCTGTATCAAAACCTACGGATGA 3341
Db 3185 ACAACCTGTCGGCCATCGAGGCCAGCAGCAGCACTGCTGACGCTGACCGTGGGGCA 3244
Qy 3342 AATTGACCTGTATTCCTATCCATCCATCGTCTCG- - - - - GCTTTCGCAAAATCACTATGGAG 3398
Db 3245 TCAAGCAGCTGAGGGCCGACCCCTGCGCTGGAGCGCTACCTGGAAGGACGACGAGC 3304
Qy 3399 TGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTCAAGTTCGTA 3458
Db 3305 TCAGCAGATCTGGAACCAACACCTGATGAGTGGAGCGGACCGGAGATCAACAACTACA 3364
Qy 3459 GGGCTTTCCCCACTGTTTGGCTTTCAGCTATATGATGATGATGTTATGGGGGCCAAGT 3518
Db 3365 CAGCCTGATCCACAGCCTGATCGAGGAGCGCAGAACCCAGCAGGAGAACGACGAGG 3424
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Db 3425 AGCTGCTGGAGCTGGCAAGTGGGCGAGCCCTGTGGAACCTGGTTCAACATCACCAACTGGC 3484
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Db 3485 TGTGTTACATCAAGCTGTTTCATCATGATCGTGGGCGCCTGGTGGGCTCGGCATCGTGT 3544
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Qy 3698 TTGTTTGGCCCTCCCGCTGCTTCTTGACCTCGAAGTGGCACTCCCACTGTCTCTT 3757
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Db 3725 GTGGGTGGGCGAGGACAGCAAGGGGAGGATTTGGGAAGACAATAGCAGGCATGCTGGG 3784
Qy 3878 AGC- - - - - 3880
Db 3785 ATGCGGTGGGCTCTATGCGGTACCCAGGTGCTGGAAGAAATTGACCCGGTTCTCTGGGCCA 3844
Qy 3881 - - - - - 3880
Db 3845 GAAAGAAGCAGGCACATCCCTTCTCTGTGACACACCTGTCCACGCCCCCTGTTCTTAG 3904
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Qy 3881 TCTTCGCTTCTCTGCTCATCTGACTCGCTGCGCTCGGTGCTGCGTGGGCGAGCGGTA 3940
Db 4145 TCTTCGCTTCTCTGCTCATCTGACTCGCTCGCTCGGTGCTGCGTGGGCGAGCGGTA 4204
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Db 4205 TCAGCTCACTCAAGGCGGTATACGGTTATCCACAGAAATCAGGGGATTAACGAGGAAAG 4264
Qy 4001 AACATGTGACAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGCCGCTGCTGGCG 4060
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Qy 4061 TTTTTCATAGGCTCGCGCCCCCTGACGAGCATCAAAAATCGACGCTCAATCGAGAG 4120
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DB |||||
QY 4565 TCCAACTGGCTGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGT 4624
DB |||||
QY 4361 AACTATCGTCTTGAAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGCGACGACCACT 4420
DB |||||
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DB |||||
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DB |||||
QY 4805 ACCTTCGGAAGAGTGTGTAGTCTCTGATCCGGCAAAACCAACCAACCGCTGTAGCGGT 4864
DB |||||
QY 4601 GGTATTTTGTGTTGCAAGCAGCAGATTACCGCGAGAAAAAAGGATCTCAAGAAGATCCT 4660
DB |||||
QY 4865 GGTATTTTGTGTTGCAAGCAGCAGATTACCGCGAGAAAAAAGGATCTCAAGAAGATCCT 4924
DB |||||
QY 4661 TTGATCTTTTACGGGGTCTGACGCTCAGTGAAGCAAAACCTCAGGTTAAGGATTTTG 4720
DB |||||
QY 4925 TTGATCTTTTACGGGGTCTGACGCTCAGTGAAGCAAAACCTCAGGTTAAGGATTTTG 4984
DB |||||
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DB |||||
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DB |||||
QY 5045 AAATCAATCTAAAGTATATAGTAAACTTGTCTGACAGTTACCAATGCTTAATCACT 5104
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QY 4841 GAGGACCTATCTCAGCGATCTGTCTATTTGTTTCAATCATAGTGTGCTGACTC 4894
DB |||||
QY 5105 GAGGACCTATCTCAGCGATCTGTCTATTTGTTTCAATCATAGTGTGCTGACTC 5158
DB |||||

RESULT 14

US-10-359-120-157
; Sequence 157, Application US/10359120
; Publication No. US20040033487A1
; GENERAL INFORMATION:
; APPLICANT: NABLE, Gary J.
; APPLICANT: CHAKRABARTI, Bimal K.
; APPLICANT: HUANG, Yue
; TITLE OF INVENTION: MODIFICATIONS OF HIV Env, Gag, AND Pol
; FILE REFERENCE: NIH206.001C1
; CURRENT APPLICATION NUMBER: US/10/359,120
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: PCT/US01/25721
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/279,257
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/252,115
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/225,097
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 6438
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid pVR1012x/s containing HIV genes
US-10-359-120-157

Query Match 38.7%; Score 2275.8; DB 17; Length 6438;
Best Local Similarity 69.5%; Pred. No. 0;
Matches 3558; Conservative 0; Mismatches 1232; Indels 333; Gaps 21;
QY 1 TCGCGGTTTCGGTGATGACGGTGAACAACTCTGACACATGCACTCCCGGAGACGGTCA 60
DB |||||
QY 1 TCGCGGTTTCGGTGATGACGGTGAACAACTCTGACACATGCACTCCCGGAGACGGTCA 60
DB |||||
QY 61 CAGCTTGTCTGAAGCGGATGCGGAGAGAGCAAGCCCGTCAAGGCGCGTCAAGCGGGTG 120
DB |||||
QY 121 TTGGCGGGTGTTCGGGCTGGCTTAACTATGCGGCATCAGACAGATTGTACTGAGAGTGC 180
DB |||||
QY 121 TTGGCGGGTGTTCGGGCTGGCTTAACTATGCGGCATCAGACAGATTGTACTGAGAGTGC 180
DB |||||
QY 181 ACCATATGAAGCTTTTTTGCAAAAGCTTAGGCCTCCAAAAAGCCTCCTCACTACTTCTGG 240
DB |||||
QY 181 ACCATATGGG-----TGGAATACCGCAC 207
QY 241 AATAGCTCAGAGCGCGAGCGGCTCTGGCTCTGTCATAATAAAAAAATTAGTCAGCCA 300
DB |||||
QY 208 GATGCGTAGGAGAAAAATACCGCATCAG-----235
QY 301 TGGGCGGAGATGGCGGAACCTGGGCGGGAGGGAATTATTGGCTATTGGCCATTGCAAT 360
DB |||||
QY 236 -----ATTGGCTATTGGCCATTGCAAT 256
QY 361 AGTTGTATCTATATCAATAATGTACATTTATATTGGCTCATGTCCAATATGACCGCCA 420
DB |||||
QY 257 AGTTGTATCCATATCAATAATGTACATTTATATTGGCTCATGTCCAATATGACCGCCA 316
QY 421 TGTGACATGATTAATGTAGTATTAATAAGTAAATCAATTAAGGGTCAATTAGTTTCA 480
DB |||||
QY 317 TGTGACATGATTAATGTAGTATTAATAAGTAAATCAATTAAGGGTCAATTAGTTTCA 376
QY 481 AGCCATATATCGAGTTCGCGTTACATAAATTTAGGTAATAAGGCGCGCTGCTGACCG 540
DB |||||
QY 377 AGCCATATATCGAGTTCGCGTTACATAAATTTAGGTAATAAGGCGCGCTGCTGACCG 436
QY 541 CCCAACGACCCCGCCCATTTGACGTCAATAATGAAGTATGTTCCCATAGTAAACCAATA 600
DB |||||
QY 437 CCCAACGACCCCGCCCATTTGACGTCAATAATGAAGTATGTTCCCATAGTAAACCAATA 496
QY 601 GGGACTTTCCATGACGTCAATAGGGTGGAGTATTACGGTAATAAGTCCCACTTTGGCAGTA 660
DB |||||
QY 497 GGGACTTTCCATGACGTCAATAGGGTGGAGTATTACGGTAATAAGTCCCACTTTGGCAGTA 556
QY 661 CATCAAGTGTATCATATGCGAGTCCGCCCTTATTGACGTCAATGACGTAATAAGTCC 720
DB |||||
QY 557 CATCAAGTGTATCATATGCGAGTCCGCCCTTATTGACGTCAATGACGTAATAAGTCC 616
QY 721 GCTGGCATTTATGCCAGTACATGACCTTTACGGGACTTTTCTTACCTTTGGCAGTACATCTAC 780
DB |||||
QY 617 GCTGGCATTTATGCCAGTACATGACCTTTACGGGACTTTTCTTACCTTTGGCAGTACATCTAC 676
QY 781 GTATTAGTCATCGCTATTACATAGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
DB |||||
QY 677 GTATTAGTCATCGCTATTACATAGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 736
QY 841 TAGCGGTTTGTACGACGGGATTTCCAGTCTCCACCCCATTTGACGTCAATGAGGTTTG 900
DB |||||
QY 737 TAGCGGTTTGTACGACGGGATTTCCAGTCTCCACCCCATTTGACGTCAATGAGGTTTG 796
QY 901 TTTTGGCACCAAAATCAACGGGACTTTCCAAATGTCTGTAATAACCCGCCCTTTGAGCG 960
DB |||||
QY 797 TTTTGGCACCAAAATCAACGGGACTTTCCAAATGTCTGTAATAACCCGCCCTTTGAGCG 856
QY 961 CAAATGGCGGTAGCGGTGTACGGTGGGAGTCTATATAGCAGAGCTGTTTAGTGAAC 1020
DB |||||
QY 857 CAAATGGCGGTAGCGGTGTACGGTGGGAGTCTATATAAGCAGAGCTGTTTAGTGAAC 916
QY 1021 CGTCAGATCGCCTGGAGAGCGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGAC 1080

[illegible]

1997	Db	GAGCTGAGCGCTTCGCGGTGAACCCCGGCGCTGCTGGAGACGAGCGGCGCTGCCGCCAG	2056
2127	Qy	GCACACGCGCCCAAGCAGAAACGTCACAGTCATCAACACCAACG-----GCAGTTGGCAC	2180
2057	Db	ATCTGGGCGCAGCTGGCAGCCAGCCTGCAGACCGGACGCGAGGAGCTGCGCAGCTGTAC	2116
2181	Qy	CTCAATAGCAGCGGCGCTGAATCTGAATGATAGCC-----TCAACACGGGCTGGTTG	2231
2117	Db	AACACCGTGGCCACCCCTGTACTCGTGCACACGCGCATCGAGATCAAGGACACCAAGGAG	2176
2232	Qy	GCAGGCGTTTCTATCACCAACAAGTTCAACTCTTCAGGCTGTCTGAGAGGCTAGCCAGC	2291
2177	Db	GCCCTGACAAGATCGAGGAGGACGACACAGACGAGAGGAGGAGGAGGAGGAGGAGGAGG	2236
2292	Qy	TGCGACCCCTTACCGATTTTGACAGGGCTGGGGCCCTATCAGTTATGTATGCAACGGAAGC	2351
2237	Db	GCCGACACCGCCACAGCAACCAAGGTAGCCAGACCTACCCCATCGTGCAGAACATCCAG	2296
2352	Qy	GGCCCCGACAGCGGCCCTTACTGCTGCGACTACCCCCCAAAACCTTGCGGTATTTGCGCC	2411
2297	Db	GGCCAGATGTCACACGAGCCATCAGCCCCCGCACCCCTGAAACGCTGGTGAAGGTGGTG	2356
2412	Qy	GCGAAGAGTGTGTGTGCTCGGTATATTGCTTCTCCAGACCCCGTGGTGGTGGGAACG	2471
2357	Db	GAGGAGAGGCCCTTCAGCCCCGAGGTGATCCCCATGTTTCAGCGCCCTGACGAGGCGGCC	2416
2472	Qy	ACCGACAGG--TCGGGCGGCCACCTACAGCTGGGGTGAAAATGATACGGACGTCTTC	2528
2417	Db	ACCCCCAGCACTGACACCATGCTGACACACCGTGGGCGGCCACGAGCGCCATGCGAG	2476
2529	Qy	GTCTTTAACAATACC---AGGCCACCGCTGGGGAATTGTTTCGGTTGTAACCTGGATGAA	2584
2477	Db	ATGCTGAAGGAGACCATCAACAGGAGGCGCGCGAGTGGGACCGCGTGCACCCCGTCAC	2536
2585	Qy	CTCAACTGAGATTACCAAAAGTGTGGGAGC--CCCTCTTGTGTCTATCGAGAGGGCGGGC	2642
2537	Db	GCGCGCCCCATCGCCCCCGCCAGATGCGCGAGCGCCGCGGACGAGCATCGCGCGGACCC	2596
2643	Qy	AACAACACCCCTGCACCTGCCCACTGATGTTCTCCGAAAGCATCCGGACGCCACATACTCT	2702
2597	Db	ACAGACCCCTGCAGGACAGATCGCTGATGACAAACACCCGCCCATCCCGCTGGGC	2656
2703	Qy	CGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCTGGTTCGACTACCCGTATAGGCTT	2762
2657	Db	GAGATCTACAAGCGCTGATCATCTCGGCGCTGAAACAAGATCGTGGCGATGTACAGCCCC	2716
2763	Qy	TGGCATATCTTGTACCATCACTACACATATTAAATCAGGATGTACGTGGGAGGG	2822
2717	Db	ACCAGCATCTTGACATCTCCCGAGGGCCCCAAGAGCCCTTCGCGCACTACGTGGACCGC	2776
2823	Qy	GTGCAACACAGGCTGGAAGCTGCTGCAACTGACGCGGGCGAAAGTTG-----	2872
2777	Db	TTCTAAGAACCCTGCGCGCGAGGAGGCGCAGCCAGAGGTGAAGAAGTGGATGACCGAG	2836
2873	Qy	--CGATCTGGAAGTAGGACAGGTCGAGATCGATATGGAGAACATCAATCAGGATTC	2930
2837	Db	ACCTGCTGTGTCAGAACGCCAACCCGACTGCAAGACCATCTCTGAAGGCCCTGGGCCCC	2896
2931	Qy	CTAGGACCCCTGCTGTGTTCAGGCGGGT-----	2961
2897	Db	GCGGCCACCCCTGGAGGAGATGATGACCGCTCGCAGGGCGTGGGCGGCCGCCCAAG	2956
2962	Qy	---TTTTTCTGTGACAGAAATCCTCAAAATACCGCAGAGCTAGACTCGTGGTGGAC	3016
2957	Db	GCCCGCGTCTGGCGGAGGCCATGAGCCAGGTGACCAACAGCGGCCCATCATGATGCGAG	3016
3017	Qy	TTCTCTCAATTTTCTAGGGGGAATCTCCGCTGTGTCTTTGGCCAAAATTCGCAAGTCCCCAAC	3076
3017	Db	CGCGGCAATCTCGCAACACGACCAAGATCGTGAAGTCTTCACTCGCGCAAGGAGGC	3076
3077	Qy	CTCAATCACTCAACACCTCTGTCTCTCAATTTTGTCTGGTTATCGCTGGATGTGTCT	3136
3077	Db	CACACCGCCGCAACTGTCGCGGCCCGCCGCAAGAAGGGCTGCTGGAAAGTCGCGCAAGGAG	3136

QY 3137 GCGCGCTTTATCATATTCCTCTTCAATCTGCTGCTATGCTCATCTTCTTATTTGTTCT 3196
DB 3137 GGCACACAGATGAAGGACTGCACCGAGCGCAGAGCTAAATTTTATGGGAAGATCTGGCCT 3196
QY 3197 TCTGGATTATCAAGG-----TATGTTGCCGCTTTGCTCTAATTTCCAGGATCAACA 3248
DB 3197 TCCCACAAGGGAAGGCGAGGGAATTTCTTACAGCAGACGAGCCAAAGCCCCACCA 3256
QY 3249 ACAACAGTACGGGACCATGCMAAACCTGCACGACTCCTGCTCA-----A 3293
DB 3257 GAAGAGAGCTTCAGGTTTGGGAAGAGACAACAACCTCCCTCTCAGAAGCAGGAGCGGATA 3316
QY 3294 GGCAACTCTATGTTTCCCTCATGTTGCTGTACAAAAC----- 3330
DB 3317 GACAAGGAATCTATCTCTTATGCTTCCCTCAGATCACTCTTTGGCAGCAGCCCCGTGCA 3376
QY 3331 -----CTACGGATGGAATTTGCACCTGTAATTCCTATCCCATCGCTGGGC 3376
DB 3377 CAATAAAGATAGGGGCGCAGCTGAAGAGGCCCTTCTAGACAGGCCCTGGATCCAGATC 3436
QY 3377 TTTTCGCAAAATACCTATGGAGTGGGCGCTCAGTCCGTTTCTCTTGGCTCAGTT----- 3429
DB 3437 TGCCTGTCCTTCTAGTTGCCAGCATCTGTTGTTTGGCCCTCCCGTGCCTTCTCTTGAC 3496
QY 3430 -----TACTAGTCCCAATTTGTTTCAGTGGTTCGTAGGGCTTTTCCCCCACTG 3474
DB 3497 CCTGGAAGGTGCCACTCCCACTGCTCTTCTTAATAAATGAGGAATTTGCATCGCATTTG 3556
QY 3475 TTTGGGCTTTCAGCTATA-----TGATGATGTTGTTATTTGGGGCCCAAGTCTGTACAGCA 3528
DB 3557 TCTGAGTAGGTGTCATTTCTATTTCTGGGGGTGGGGTGGGGCAGGACAGCAAGGGGAGGA 3616
QY 3529 TCGTAGTCCCTTTATACCGCTTTACCAATTTTCTTTGCTCTCGGTATATCATTTAAG 3588
DB 3617 TTGGGAAGACAATAGCAGGCATGCTGGGATGCGTGGGCTCTATGGGTACCCAGGTCT 3676
QY 3589 AA-----TTACAGCTCAGCAAGTCTAGAAAGGCGCCCAAGATATCAAGGA 3635
DB 3677 GAAGAAATGACCCGGTTCTCTCGGGCCAGAAAGAGCAGGCACATCCCTCTCTGTGA 3736
QY 3636 TCCACTACGGTTAGAGTCCGTGATCAGCTCAGCTGTCCTTCTAGTTGCCAGCCATC 3695
DB 3737 CACACCTGTCCACGCCCTGTTCTTAGTTCCAGCCCACTCATAGGACACTCATAGCT 3796
QY 3696 TGTGTTTGGCCCTCCCGCTGCTTCTTGACCTCGGAAGTGCACCTCCCACTGCTCT 3755
DB 3797 CAGGAGGCTCCGCTTCAATCCACCCGCTAAAGTACTTTGGAGCGGTCTCTCCCTCCT 3856
QY 3756 TTTCTTAATAATGAGGAATTCATCGCATTTGCTGAGTAGGTGTCATTTCTTTGCGG 3815
DB 3857 CATCAGCCCAACCAACCTAGCTCCAGAGTGGGAAGAAATTAAGCAAGATAGG 3916
QY 3816 GGGTGGGTGGGCGAGCAGCA-----AGGGGAGGATTG 3851
DB 3917 CTATTAAAGTGCAGGGGAGAGAAATGCTTCCAAATGTGAGGAATGATGAGAAATC 3976
QY 3852 GGAAGACAATAGCAGGCATGCTGGGAGCTCTTCCGCTTCTCGCTCACTGACTCGCTGC 3911
DB 3977 ATAGAATTTTAAGGCCATCATGSCCTTAATCTTCCGCTTCTCGCTCACTGACTCGCTGC 4036
QY 3912 GCTCGTGTGCTGGCTCGGCGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGTTAT 3971
DB 4037 GCTCGTGTGCTGGCTCGGCGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGTTAT 4096
QY 3972 CCACAGAACTCAGGGGATAACGAGGAAGAACATGTAGCAAGGCCAGCAAGGCCCA 4031
DB 4097 CCACAGAACTCAGGGGATAACGAGGAAGAACATGTAGCAAGGCCAGCAAGGCCCA 4156
QY 4032 GGAACCGTAAAAAGGCGCGTCTGCTGGCGTTTTTCCATAGGCTTCCGCCCTCCCTGACGAGC 4091
DB 4157 GGAACCGTAAAAAGGCGCGTCTGCTGGCGTTTTTCCATAGGCTTCCGCCCTCCCTGACGAGC 4216

QY 4092 ATCAGAAAATCGACGCTCAAGTCAAGTGTGGGAAACCCGACAGACTATATAAGATACC 4151
DB 4217 ATCAGAAAATCGACGCTCAAGTCAAGTGTGGGAAACCCGACAGACTATATAAGATACC 4276
QY 4152 AGGCGTTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCG 4211
DB 4277 AGGCGTTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCG 4336
QY 4212 GATACCTGTCGCTTTCTCTTCCGGAAGCGTGGCGCTTTCTCAATGCTCACTGCTGA 4271
DB 4337 GATACCTGTCGCTTTCTCTTCCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGA 4396
QY 4272 GGTATCTCAGTTGCGGTAGTGTCTGCTCAAGCTGGCTGTGTCAGCAACCCCGG 4331
DB 4397 GGTATCTCAGTTGCGGTAGTGTCTGCTCAAGCTGGCTGTGTCAGCAACCCCGG 4456
QY 4332 TTTAGCCCCAGCGCTGCGCTTTATCCGCTTAACTATCTGCTTGAAGTCCAAACCCGGTAAAGAC 4391
DB 4457 TTTAGCCCCAGCGCTGCGCTTTATCCGCTTAACTATCTGCTTGAAGTCCAAACCCGGTAAAGAC 4516
QY 4392 AGACTTATTCGCACTGGCAGCAGCCACTGGTAAACAGGATTAAGCAGAGAGGTATGTAG 4451
DB 4517 AGCACTTATTCGCACTGGCAGCAGCCACTGGTAAACAGGATTAAGCAGAGAGGTATGTAG 4576
QY 4452 GCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGCTACACTAGAGCAGAGTAT 4511
DB 4577 GCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGCTTGAAGCAGAGTAT 4636
QY 4512 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTGGAAAAAGAGTTGCTAGCTCTTGAT 4571
DB 4637 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTGGAAAAAGAGTTGCTAGCTCTTGAT 4696
QY 4572 CCGGCAAAACAAACCCGCTGCTAGCGGTGTTTTTTGTTTGGCAAGCAGAGATTAACGC 4631
DB 4697 CCGGCAAAACAAACCCGCTGCTAGCGGTGTTTTTTGTTTGGCAAGCAGAGATTAACGC 4756
QY 4632 GCAGAAAAAAGAGTCTCAAGAGATCTTTGATCTTTCTACGGGTCTGACGCTCAGT 4691
DB 4757 GCAGAAAAAAGAGTCTCAAGAGATCTTTGATCTTTCTACGGGTCTGACGCTCAGT 4816
QY 4692 GGAAGCAAACTCAGCTTAAAGGATTTTGGTCTAGAGATTTCAAAAAGGATCTTCACT 4751
DB 4817 GGAAGCAAACTCAGCTTAAAGGATTTTGGTCTAGAGATTTCAAAAAGGATCTTCACT 4876
QY 4752 AGATCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATAGTAAACTT 4811
DB 4877 AGATCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATAGTAAACTT 4936
QY 4812 GGTCTGACAGTTACCAATGCTTAAATCAGTGAGCAGCTTATCTCAGCGATCTGTCTATTTC 4871
DB 4937 GGTCTGACAGTTACCAATGCTTAAATCAGTGAGCAGCTTATCTCAGCGATCTGTCTATTTC 4996
QY 4872 GTTTCATCCATAGTTGCTGACTC 4894
DB 4997 GTTTCATCCATAGTTGCTGACTC 5019

RESULT 15

US-10-359-120-32
; Sequence 32, Application US/10359120
; Publication No. US20040033487A1
; GENERAL INFORMATION:
; APPLICANT: NABLE, Gary J.
; APPLICANT: CHAKRABARTI, Bimal K.
; APPLICANT: HUANG, Yue
; TITLE OF INVENTION: MODIFICATIONS OF HIV Env, Gag, AND Pol
; TITLE OF INVENTION: ENHANCE IMMUNOGENICITY FOR GENETIC IMMUNIZATION
; FILE REFERENCE: NIH206.001C1
; CURRENT APPLICATION NUMBER: US/10/359,120
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: PCT/US01/25721
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/279,257

677	QY	GTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGCGGTGGA	736
841	QY	TAGCGGTTTTGACTCACGGGGAATTCGAAGTCTCCAGCTCCACCCCAATGACGTCGAATGGAGTTTG	900
737	DB	TAGCGGTTTTGACTCACGGGGAATTCGAAGTCTCCAGCTCCACCCCAATGACGTCGAATGGAGTTTG	796
901	QY	TTTTGGCACCAAAATCAAAGGACCTTTCCAAAATGTCGTAATAAACCCCGCCCGCTTGACG	960
797	DB	TTTTGGCACCAAAATCAAAGGACCTTTCCAAAATGTCGTAATAAACCCCGCCCGCTTGACG	856
961	QY	CAAATGGGCGGTAGGCGGTGTCGGTGGGAGGTCCTATATAAGCAGAGAGCTCGTTTTAGTGAAC	1020
857	DB	CAAATGGGCGGTAGGCGGTGTCGGTGGGAGGTCCTATATAAGCAGAGAGCTCGTTTTAGTGAAC	916
1021	QY	CGTCAGATCGCTGGAGACGCCAATCAACGCTGTTTTGACCTCTCATAGAGACACCGGAC	1080
917	DB	CGTCAGATCGCTGGAGACGCCAATCAACGCTGTTTTGACCTCTCATAGAGACACCGGAC	976
1081	QY	CGATCCAGCCTCCGCGCGCGGGAACGGTGCATTTGGAAACGGGATTCGCCGTGGCAAGAGT	1140
977	DB	CGATCCAGCCTCCGCGCGCGGGAACGGTGCATTTGGAAACGGGATTCGCCGTGGCAAGAGT	1036
1141	QY	GAGCTAAGTACCGCCTATAGACTCTATAGCACACCCCTTTGGCTCTTATGCAATGCTATA	1200
1037	DB	GAGCTAAGTACCGCCTATAGACTCTATAGCACACCCCTTTGGCTCTTATGCAATGCTATA	1096
1201	QY	CTGTTTTTGGCTTTGGGGCCCTATACACCCCGC - TCCTTATGCTATAGGTGATGCTATAGC	1259
1097	DB	CTGTTTTTGGCTTTGGGGCCCTATACACCCCGCTTCCTTATGCTATAGGTGATGCTATAGC	1156
1260	QY	TTAGCCTATAGGTGCGGTTATTTGACCAATATTGACCACTCCGCCCTATTGGTGAAGTACT	1319
1157	DB	TTAGCCTATAGGTGCGGTTATTTGACCAATATTGACCACTCCGCCCTATTGGTGAAGTACT	1216
1320	QY	TTCCATTACTTAATCAATAATGGCTCTTTGGCACAACTATCTCTATGCTATATGCGCA	1379
1217	DB	TTCCATTACTTAATCAATAATGGCTCTTTGGCACAACTATCTCTATGCTATATGCGCA	1276
1380	QY	ATACTCTGCTCTTTCAGAGACTGACACGGACTCTCTGTAATTTTTACAGGATGGGCT - CCATTT	1438
1277	DB	ATACTCTGCTCTTTCAGAGACTGACACGGACTCTCTGTAATTTTTACAGGATGGGCTCTT	1336
1439	QY	ATTATTTCAAATTCATATACAAAGCGCGTCCCGGTGCGCGGAGTTTTTTATTTAA	1498
1337	DB	ATTATTTCAAATTCATATACAAAGCGCGTCCCGGTGCGCGGAGTTTTTTATTTAA	1396
1499	QY	CATAGCGTGGATCTCC --- GACATCTCGGTAACGTTCCGAGACATGGGCTCTCTCCG	1555
1397	DB	CATAGCGTGGATCTCCAGCGGAATCTCGGGTACGTTCCCGACATGGGCTCTCTCCG	1456
1556	QY	GTACGCGCGGAGCTTCCACATCCGAGCCTGTGTCCTATCCGTCAGCGGCTCATGTGCG	1615
1457	DB	GTACGCGCGGAGCTTCCACATCCGAGCCTGTGTCCTATCCGTCAGCGGCTCATGTGCG	1516
1616	QY	TCGGCAGCTCTTGTCTCTAAAGTGGAGCCAGACTTTAGGCAACAGCAATGCCACCA	1675
1517	DB	TCGGCAGCTCTTGTCTCTAAAGTGGAGCCAGACTTTAGGCAACAGCAATGCCACCA	1576
1676	QY	CCACCAAGTGGCGCAACAGGCGGTGCTGAGGATGCTGCTGTAATATGACTCGGAG	1735
1577	DB	CCACCAAGTGGCGCAACAGGCGGTGCTGAGGATGCTGCTGTAATATGACTCGGAG	1636
1736	QY	ATTGGGCTCGACCTG - GACGCAAGATGGAAGACTTAAGGCAGCGGCAAGAGAAGATGCGAG	1794
1637	DB	ATTGGGCTCGACCGCTGACGCAATGGAAGACTTTAAGGCAAGGCGGCAAGAGAAGATGCGAG	1696
1795	QY	GCAGCTGAGTTGTTATTCTGATAAGAGTCAAGAGTAACTCCCGTTGCGGCTCTGTTAA	1854
1697	DB	GCAGCTGAGTTGTTATTCTGATAAGAGTCAAGAGTAACTCCCGTTGCGGCTCTGTTAA	1756
1855	QY	CGGTGAGGCGAGTGTAGTCTGACAGATCTCGTTCTGCGCGCGCGGCAACAGACATA	1914
1757	DB	CGGTGAGGCGAGTGTAGTCTGACAGATCTCGTTCTGCGCGCGCGGCAACAGACATA	1816

QY 1915 ATAGCTGACAGACTAAGAGCTGTTCCCTTTCCATGGGTCTTTTCTCGAGTACCCGTCGTC 1974
DB |||||
1817 ATAGCTGACAGACTAAGAGCTGTTCCCTTTCCATGGGTCTTTTCTCGAGTACCCGTCGTC 1876
QY |||||
1975 GACGAATTCAAGCAATCATGGATG-----CAATGAAGAGAGGGCTCTGCTGTGCTGCT 2029
DB |||||
1877 GACCGTGTGATCAGATATCGCGGCGCTCTAGAAATGCGCGTGAAGGAGAAGTACCAGCA 1936
QY |||||
2030 GCTGTGTGGAGCAGTCTTGCTTTGCGCCAGCGCTAGCGAAACCCACGTCACCGGGGGAAG 2089
DB |||||
1937 CTTGTGCGCTGGGGCTGGCGCTGGGCAACCATGCTGCTGGGCATCTGATGATCTGCAG 1996
QY |||||
2090 TGGCGGCGCACACTGTGCTGTGATTTGTTAGCTCTCTCGACACAGGCGCCCAAGCAGAAGCT 2149
DB |||||
1997 CGCCACCGAGAAGCTGTGGGTGACCTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAC 2056
QY |||||
2150 CCAGCTGATCAACACCAAGGAGTTGGCACCTCAATAGCAGCGCCCTGAACTGCAATCA 2209
DB |||||
2057 CACCACCTTGCTCTGCGCCAGCGACGCCAAGGCTACGACCCGAGGTGCA---CAACGT 2113
QY |||||
2210 TAGCCTCAACACCGGTGTGGCAGGGCTTTTCTATCACCAAGTTTCAACTCTTTGAG 2269
DB |||||
2114 GTGGCCACCCAGCGCTGCGTCCACCGACCCCAACCCAGGAGGTGCTGTGTGAA 2173
QY |||||
2270 CTGTCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGAACAGGGCTGGGGCCC 2329
DB |||||
2174 CGTGACCGAGAATCTCGACATGTGGGAAGAACGACATGCTGGAGCAGATGACGAGACAT 2233
QY |||||
2330 TATCAGTTATGCCAAGGAGGGCCCCGACGAGCGCCCTACTGCTGGCAGCTACCCCC 2389
DB |||||
2234 CATCA-----GCTGTGGACCAAGAGCCCTGAGGCCCTGCGTAAGCTGACCCCCCTGTGC 2288
QY |||||
2390 AAAACCTTGGGTATTGTGCCCGCAAGAGTGTGTGTCGCGTATATTGTTCTCACTCC 2449
DB |||||
2289 GTGAGCTGAAGTGACCG-AGCTAGCAAGAACTGCAGCTTCAACATCAGCACACAGCAT 2347
QY |||||
2450 CAGCCCGTGTGTGGGAAGAACGACGACAGTGTGGGCGGCCACCTACAGCTGGGGTGA 2509
DB |||||
2348 CCGCGCAAGGTGCAGAAGGATGACCGCTTCTTCTACAAGCTGGACATATCCCCATCGA 2407
QY |||||
2510 AAATGATACGGAAGTCTTCTGCTTAAACAATACGAGCCAGCGCTGGGCAATTGGTTGCG 2569
DB |||||
2408 CAAAGCACACACAGCTACAGCTGACAGCTGACGCTGCAACACACAGGCTGATCACCCAG--GC 2464
QY |||||
2570 TTGTACTTGGATGAATCAACTGGAATTCACCAAGTGTGGGAGCGCCTCTTGTGTGAT 2629
DB |||||
2465 CTGCCCAAGGTGAGCTTCGAGGCCATCCCAACCACTACTGCGCCCCCGCGCTTGC 2524
QY |||||
2630 CGGAGGGCGGGCAACAAACCTGCACTGCCCCCACTGATTTGTTCCGCAAGCATCCGGA 2689
DB |||||
2525 CATCTGAAAGTGCAGGACAAAGATTCAACGCGCAAGGGCCCCCTGCACCAACGTGAGCAC 2584
QY |||||
2690 CGCCACATCTCTCGGTGGGGTCCGGTCCCTGGATCACAC-----CCAGGTG 2737
DB |||||
2585 CGTGAGTGCACCCACGGCATCCGCCCCGTGTGTGAGCACCCAGCTGCTGCTGAACGGTAG 2644
QY |||||
2738 CTTGTGCTGACTACCCGTATAGGCTTTGGCATTTATCTTGTATCCCTTGTACCATCAACTACACCAATT 2797
DB |||||
2645 CTTGGCCGAGGAGGAGTGTGATCCGAGCGCTAACTTCCGCGCAACCGCAAGGTGAT 2704
QY |||||
2798 TAAATCAGATGTAGTGGAGGGGTGAAACACAGGCTGGAAGCTGCTGCAACTGGAC 2857
DB |||||
2705 CATGTGTCAGCTGAACGAGAGCGTGGAGATCACTGACCCGCGCTTAGCGCCCACTGCAA 2764
QY |||||
2858 GCGGGCGGAAGCTTGGCATCTGGAAGATAGGGACAGTCCGAGATCGATATG-GAGAAACA 2916
DB |||||
2765 CTTGAGCCGGGCCAAGTGGAAAGACACCTCTGAACAGATCTGTGATCAAGCTGCGCGAGCA 2824
QY |||||
2917 TCACATCAGATTCTAGGACCCCTGCTGTGTATTACAGCGGGGGTTTTTTCTTTGTGACAA 2976
DB |||||
2825 GTTGGCAACAAGACCATCGTGTTCAGACACAGCAGCGGGCGGCGACCCCGAGATCTGTAC 2884

QY 2977 GAATCTCACAATACCGCAGAGCTTAGACTCGTGGTGAGTCTCTCTCAATTTTCTAGGGG 3036
DB |||||
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QY |||||
3037 GATCTCCCGTGTCTTTGGCCAAAATTCGCAGTCCCAACCTCCCAATCACTCAACCAACCT 3096
DB |||||
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QY |||||
3097 CTTGCTCTCCAAATTTGCTCTGGTTATCGCTGAGATGTCTGGGGCTTTTATCATATTC 3156
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QY |||||
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DB |||||
3124 GCGCAGCGAGCTGTACAGTACAGGTGGTGAAGATCGAGCCC-----CTGGGCG 3174
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DB |||||
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QY |||||
3874 GGGGAGC----- 3880
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QY ----- 3880
3828 GCCAGAAAGACGAGCACAATCCCTTCTCTCTGTGACACACCTGTCTCCACGCCCTGTTTC 3887
QY ----- 3880
3888 TTAGTTCCAGCCCCCTCATATAGGACACTCATAGCTCAGGAGGGCTCCGCCCTTCAATCCCA 3947
DB ----- 3880
3881 ----- 3880

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Db	4068	TGCCTCCAACATGTGAGGAAGTAATGAGAGAAATCATAGAATTTTAAGGCCATGATTTAA	4127
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Db	4128	GGCCATCATGCCCTTAATCTTCGGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTTC	4187
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Db	4308	AGGCCGGTGTCTGGGGTTTTTCCATAGGCTCCGCCCTCCCTGACGAGCATCAAAAAATC	4367
Qy	4104	GACGCTCAAGTACAGAGTGGCGAAACCCGACAGAGCTATAAAGATACCAAGCGGTTCCTCC	4163
Db	4368	GACGCTCAAGTACAGAGTGGCGAAACCCGACAGAGCTATAAAGATACCAAGCGGTTCCTCC	4427
Qy	4164	CTGGAAAGCTCCCTCGTGGGCTCTCTCTGTTCCGACCTTACCGGATACCTGTGCG	4223
Db	4428	CTGGAAAGCTCCCTCGTGGGCTCTCTCTGTTCCGACCTTACCGGATACCTGTGCG	4487
Qy	4224	CTTTCTCCCTTCGGGAAGCGTGGGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTT	4283
Db	4488	CTTTCTCCCTTCGGGAAGCGTGGGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTT	4547
Qy	4284	CGGTGTAGGTCTCGCTCAAGCTGGGCTGTGACAGAACCCCGCTTACGCCGACC	4343
Db	4548	CGGTGTAGGTCTCGCTCAAGCTGGGCTGTGACAGAACCCCGCTTACGCCGACC	4607
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Db	4608	GCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACAGCTTATCGC	4667
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Qy	4584	CCACCCGTGGTACGGTGGTTTTTTTGTTCGAAAGCAGAGATTACCGCAGAAAAAAG	4643
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Qy	4644	GATCTCAAGAGATCTTTGATCTTTTACGGGGTCTGACGCTCAGTGGAAAGAACT	4703
Db	4908	GATCTCAAGAGATCTTTGATCTTTTACGGGGTCTGACGCTCAGTGGAAAGAACT	4967
Qy	4704	CACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAAGGATCTTACCTAGATCTTTTAA	4763
Db	4968	CACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAAGGATCTTACCTAGATCTTTTAA	5027
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Db	5028	ATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTT	5087
Qy	4824	ACCAATGCTTAATCAGTGAGGACCTATCTCAGGATCTGCTATTTTCGTTTCATCCATAG	4883
Db	5088	ACCAATGCTTAATCAGTGAGGACCTATCTCAGGATCTGCTATTTTCGTTTCATCCATAG	5147
Qy	4884	TTGCCTGACTC	4894
Db	5148	TTGCCTGACTC	5158

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Job time : 3237 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 21:50:43 ; Search time 16330 Seconds
(without alignments)

13710.596 Million cell updates/sec

Title: US-10-715-665-6

Perfect score: 5882

Sequence: 1 tcgcgcgttcggtgatgac.....tatcacgagcccttcgcg 5882

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1052.6	17.9	1070	1	AJ281552 4A3A-P6F1
2	1015	17.3	1048	7	CO552396 ACly4_50
3	986.4	16.8	1013	4	BM438846 IPLvr0015
4	920.8	15.7	1004	1	AJ281480 4A3A-P4G8
5	886.6	15.1	928	7	CO487414 GQ0227.B7
6	876.4	14.9	902	7	CR753463 DXFZp469G
7	875.8	14.9	935	4	BG838279 Gc01_10e0
8	841	14.3	841	1	AL042026 DXFZp434E
9	824.6	14.0	854	4	BM438950 IPLvr0049
10	817	13.9	865	7	CK125894 BBS182411
11	814.4	13.8	1126	8	BZ577702 msh2_5533
12	809.4	13.8	856	7	CN823189 Oa splbn
13	808	13.7	819	6	CD649375 CvGn0008
14	797.6	13.6	1011	8	BZ576726 msh2_5071
15	795.6	13.5	820	7	CR753457 DXFZp469P
16	793	13.5	827	7	CN823902 Oa splbn
17	791.8	13.5	806	4	BJ684280 BJ684280
18	782.2	13.3	1574	8	BZ572566 msh2_2693
19	774.8	13.2	1336	8	BZ575810 msh2_4637
20	774.6	13.2	800	1	AJ281449 4A3A-P4D5
21	774.4	13.2	789	6	CD280920 G4424.42
22	773.2	13.1	1370	8	BZ571721 msh2_2025
23	772.6	13.1	1073	7	CF269652 Fcylcol8
24	771.4	13.1	832	7	CN822433 Oa splbn

25	766.4	13.0	846	7	CV468077
26	765.8	13.0	769	7	CV224987
27	763.2	13.0	780	5	BQ825693
28	763.2	13.0	1249	8	BZ572284 msh2_2572
29	758.2	12.9	966	8	BZ570738 msh2_1513
30	757	12.9	759	6	CD279661 G43818.35
31	755.4	12.8	1463	8	BZ571475 msh2_1906
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38	741.4	12.6	758	9	CL422788 AB0544.Sa
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45	730	12.4	811	9	ATH517156 Arabidops

ALIGNMENTS

RESULT 1	AJ281552	1070 bp	mRNA	linear	EST 30-JUN-2000
LOCUS	4A3A-P6F11-F	Anopheles gambiae	immune competent	4A3A	Anopheles gambiae cDNA clone 4A3A-P6F11, mRNA sequence.
DEFINITION	AJ281552	EST			
ACCESSION	AJ281552.1	GI:6929432			
VERSION					
KEYWORDS	Anopheles gambiae	(African malaria mosquito)			
SOURCE	Anopheles gambiae				
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.				
REFERENCE	1 (bases 1 to 1070)				
AUTHORS	Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C., Donohue,M., Schultz,J., Benes,V., Borik,P., Ansorge,W., Soares,M.B. and Kafatos,F.C.				
TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)				
MEDLINE	20300950				
PUBMED	10841561				
COMMENT	Contact: Dimopoulos G Fotis C. Kafatos Laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany. Location/Qualifiers 1. .1070 /organism="Anopheles gambiae" /mol_type="mRNA" /strain="4A r/r" /db_xref="taxon:7165" /clone="4A3A-P6F11" /cell_line="immune competent 4A3A" /lab_host="E. coli DH10B" /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."				
FEATURES	source				
ORIGIN					

Query Match		17.9%;	Score 1052.6;	DB 1;	Length 1070;
Best Local Similarity		99.5%;	Pred. No. 5.5e-309;		
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QY	4232	CCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTTCGGGTAG	4291		
DB	181	CCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTTCGGGTAG	240		
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DB	301	TTATCCGCTAACTATCGTCTTGAGTCCAAACCGGTAAAGACAGACTTATCGCACTGGCA	360		
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DB	361	GCAGCCACTGGTAAACAGGATTAAGCAGCGAGTATGTAGGGGTGCTACAGATTCTTG	420		
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DB	601	GAAGATCTTTTATCTTTTCTACGGGGTCTGACGCTCAGTGGAAAGAAATCTCAGTTAA	660		
QY	4712	GGGATTTTGGTCTAGATATCAAAAAGGATCTTCACTAGATCTCTTTTAAATTAATAA	4771		
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DB	721	TGAAGTTTAAATCAATCTAAAGTATATAGTAAACTTTGTTGACAGTTTACCAATGC	780		
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QY	4952	ATGATACCGGAGACCCAGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCC	5011		
DB	901	ATGATACCGGAGACCCAGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCC	960		
QY	5012	GGAAGGGCCGAGCGAGAGTGGTCTGCAACTTTATCCGCTTCCATCCAGTCTATTAT	5071		
DB	961	GGAAGGGCCGAGCGAGAGTGGTCTGCAACTTTATCCGCTTCCATCCAGTCTATTAT	1019		
QY	5072	TGTTCCGGGAAGCTAGATAGTAGTTCGCCAGTTTAAATAGTTTGGCAAC	5122		

Db	1020	TGTTGCCGGGAAGCTAGAGTAAGTAGTTCCCGAGTTAATAGTTTGGCCAAC	1070	
RESULT 2				
LOCUS	CO552396	1048 bp	mRNA	linear EST 01-SEP-2004
DEFINITION	Acly4_50 Sea lamprey AcLy Petromyzon marinus cDNA, mRNA sequence.			
ACCESSION	CO552396			
VERSION	CO552396.1	GI:51800732		
KEYWORDS	EST.			
SOURCE	Petromyzon marinus (sea lamprey)			
ORGANISM	Petromyzon marinus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; Petromyzontiformes; Petromyzontidae; Petromyzon.			
AUTHORS	1 (bases 1 to 1048)			
TITLE	Pancer, Z., Mayer, W.E., Klein, J. and Cooper, M.D.			
JOURNAL	Prototypic T-cell receptor and CD4-like coreceptor expressed in lymphocytes of the agnathan sea lamprey			
COMMENT	Proc. Natl. Acad. Sci. U.S.A. 101, 13273-13278 (2004) Contact: Pancer, Zeev Division of Developmental and Clinical Immunology The University of Alabama at Birmingham 378 Wallace Tumor Institute, 1530 Third Avenue, South, Birmingham, AL 35294-3300 Tel: 205-975-5812 Fax: 205-975-7218 Email: zpancer@uab.edu.			
FEATURES	Location/Qualifiers			
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	/db_xref="taxon:7757"			
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	/dev_stage="immune stimulated larvae"			
	/clone_lib="Sea lamprey Acly"			
	/note="Vector: pGEM-T Easy; lymphocyte mRNA ESTs from PCR subtracted cDNA libraries of immune stimulated larvae. All are single pass 5' or 3' sequences randomly cloned in pGEM-T Easy (Promega)."			
ORIGIN				
	Query Match	17.3%;	Score 1015;	DB 7; Length 1048;
	Best Local Similarity	99.0%;	Pred. No. 1.7e-297;	
	Matches 1041;	Conservative	1; Mismatches 6; Indels 3; Gaps 2;	
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QY	4048	CGCGTTGCTGGCGTTTTTCATAGGCTCGCGCCCTGACGAGCATCAAAAATCGACG	4107	
Db	61	CGCGTTGCTGGCGTTTTTCATAGGCTCGG -CCCGCTGACGAGCATCAAAAATCGACG	119	
QY	4108	CTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACACAGCGTTTCCCGCTGG	4167	
Db	120	CTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACACAGCGTTTCCCGCTGG	179	
QY	4168	AAGCTCCCTCGTGGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCGCTT	4227	
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QY	4228	TCTCCCTTCGGGAAAGCGTGGCGTTTTCTCAATGCTCAAGTCTAGGTATCTCAGTTTCGGT	4287	
Db	240	TCTCCCTTCGGGAAAGCGTGGCGTTTTCTCAAGTCAAGTCTAGGTATCTCAGTTTCGGT	299	
QY	4288	GTAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCCGACCGCTG	4347	
Db	300	GTAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCCGACCGCTG	359	
QY	4348	CGCCTTATCCGGTAACTATTCGTCTTGGTCCAAACCCCGGTAAAGACAGCACTTATCGCACT	4407	
Db	360	CGCCTTATCCGGTAACTATTCGTCTTGGTCCAAACCCCGGTAAAGACAGCACTTATCGCACT	419	

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Db 420 GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCAGGATGTAGTGGCGGTGCTACAGAGTT 479
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QY 4888 CTGACTCCCGCTCGTGTAGATACTAGATACGGGGGCTTACCATCTGCGCCCGAGTGC 4947
Db 898 CTGACTCCCGCTCGTGTAGATACTAGATACGGGGGCTTACCATCTGCGCCCGAGTGC 957
QY 4948 TGAATGATACCGCGAGACCCAGCTCACCGGCTCCAGATTTATCAGCAATAAACACAGCC 5007
Db 958 TGAATGATACCGCGAGACCCAGCTCACCGGCTCCAGATTTATCAGCAATAAACACAGCC 1017
QY 5008 AGCGGAAGGGCGAGCGCAGAGTGTCT 5038
Db 1018 AGCGGAAGGGCGAGCGCAGAGTGTCT 1048
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RESULT 3

BM438846/c
LOCUS
DEFINITION 1013 bp mRNA linear EST 31-JAN-2002
IPLVr00157 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
sequence.

ACCESSION BM438846

VERSION BM438846.1 GI:18460568

KEYWORDS EST.

SOURCE Ictalurus punctatus (channel catfish)

ORGANISM
Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.

REFERENCE 1 (bases 1 to 1013)

AUTHORS Feng, J., Kucuktas, H., Kocabas, A., Li, P. and Liu, Z.

TITLE Transcriptome of channel catfish (Ictalurus punctatus): initial

analysis of expressed sequence tags from the liver

JOURNAL Unpublished (2002)

COMMENT Contact: Liu ZJ

The Fish Molecular Genetics and Biotechnology Laboratory,

Department of Fisheries and Allied Aquacultures and Program of Cell

and Molecular Biosciences

Auburn University

203 Swingle Hall, Auburn University, Auburn, AL 36849, USA

Tel: 334 844 4054

Fax: 334 844 9208

Email: zliu@acesag.auburn.edu

Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
1..1013
/organism="Ictalurus punctatus"
/mol_type="mRNA"
/db_xref="taxon:7998"
/clone_lib="Liver cDNA library"
/notes="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

ORIGIN

Query Match 16.8%; Score 986.4; DB 4; Length 1013;
Best Local Similarity 99.5%; Pred. No. 9.2e-289;
Matches 1009; Conservative 1; Mismatches 2; Indels 2; Gaps 2;
QY 4625 ATTACCGCAGAAAAAGAGCTCTCAAGAGATGCTTTCGATCTTTTCTACGGGTCTGAC 4684
Db 1013 ATTACCGCAGAAAAAGAGATCTCAAGAGATGCTTTCGATCTTTTCTACGGGTCTGAC 954
QY 4685 GCTCAGTGAACGAAAACTCACGTTAAGGATTTTGGTTCATGAGATTATCAAAAAGGATC 4744
Db 953 GCTCAGTGAACGAAAACTCACGTTAAGGATTTTGGTTCATGAGATTATCAAAAAGGATC 894
QY 4745 TTCACCTAGATCCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATAGAG 4804
Db 893 TTCACCTAGATCCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATAGAG 834
QY 4805 TAAACTTGGTCTGACAGATTTACCAGTCTTAATCAGTGAGGCACCTATCTCAGCGATCTGT 4864
Db 833 TAAACTTGGTCTGACAGTCTTAATCAGTGAGGCACCTATCTCAGCGATCTGT 774
QY 4865 CTATTTTCGTTTCATCCATAGTTGCTGACCTCCCGTCTGTAGATAACTACGATACGGGAG 4924
Db 773 CTATTTTCGTTTCATCCATAGTTGCTGACCTCCCGTCTGTAGATAACTACGATACGGGAG 714
QY 4925 GGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAGACCCAGCTCACGGTCTCCA 4984
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QY 4985 GATTTATCAGCAATAAACCCAGCCGAGGCGCGAGAGAGTGTCTCTGCAACT 5044
Db 653 GATTTATCAGCAATAAACCCAGCCGAGGCGCGAGAGAGTGTCTCTGCAACT 594
QY 5045 TTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGTAGTGTGCGCCA 5104
Db 593 TTATCCGCTCCATCCAGTCTATTAAATTTGTCGGGAAAGCTAGAGTAGTGTGCGCCA 534
QY 5105 GTTAATAGTTTGGCAACGTTGTCATTTGCTTACAGGCATCTGTGTGTCACGCTCGTCG 5164
Db 533 GTTAATAGTTTGGCAACGTTGTCATTTGCTTACAGGCATCTGTGTGTCACGCTCGTCG 474
QY 5165 TTTGGTATGGCTTCATTTCAGCTCCGCTTCCCAACGATCAAGCGAGTTTACA-TGATCCCC 5223
Db 473 TTTGGTATGGCTTCATTTCAGCTCCGCTTCCCAACGATCAAGCGAGTTTACA-TGATCCCC 414
QY 5224 CATGTTGTCAAAAAAGCGTTAGCTCTTCGCTCTCCGATCGTTGTTCAGAAAGTAGTT 5283
Db 413 CATGTTGTCAAAAAAGCGTTAGCTCTTCGCTCTCCGATCGTTGTTCAGAAAGTAGTT 355
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Db 354 GGCCGAGTGTTCATCTCATGTTATGACAGCATCTGCATAATTCCTTACTCTCATGCC 295
QY 5344 ATCCGTAAGATGCTTTTCTGTGATCTGGTGTCTCAACCAAGTCTTCTGAGAAATAGTG 5403
Db 294 ATCCGTAAGATGCTTTTCTGTGATCTGGTGTCTCAACCAAGTCTTCTGAGAAATAGTG 235
QY 5404 TATGCGGCGACCGAGTGTCTTCTTGGCCGCGCTCAATACGGGATAATAACCGCGCACATAG 5463
Db 234 TATGCGGCGACCGAGTGTCTTCTTGGCCGCGCTCAATACGGGATAATAACCGCGCACATAG 175
QY 5464 CAGAACTTTAAAGTGTCTCATCTTTCGAAAAACGTTCTTCGGGCGGAAAACTCTCAAGGAT 5523
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Db	174	CAGAACTTTAAAGTGCTCATCATTCGAAAAAGTTCTTCGCGGCGAAAACTCTCAAGGAT	115
Qy	5524	CTTACCGCTGTTGAGATCCAGTTTCGATGTAACCACTCGTGCACCAACTGATCTTCAGC	5583
Db	114	CTTACCGCTGTTGAGATCCAGTTTCGATGTAACCACTCGTGCACCAACTGATCTTCAGC	55
Qy	5584	ATCTTTTACTTTCACACAGGGTTCTCGGTGAGCAAAAACAGGAAGCAGAAATGC	5637
Db	54	ATCTTTTAACTTTACACAGGGTTCTCGGTGAGCAAAAACAGGAAGCAGAAATGC	1
RESULT 4			
AJ281480			
LOCUS	AJ281480	1004 bp mRNA linear	EST 30-JUN-2000
DEFINITION	4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P4G8, mRNA sequence.		
ACCESSION	AJ281480		
VERSION	AJ281480.1	GI:6929360	
KEYWORDS	EST.		
SOURCE	Anopheles gambiae (African malaria mosquito)		
ORGANISM	Anopheles gambiae		
REFERENCE	1 (bases 1 to 1004)		
AUTHORS	Dimopoulos, G., Caaevant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Borke, P., Ansorge, W., Soares, M.B. and Kafatos, F.C.		
TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624		(2000)
MEDLINE	20300950		
PUBMED	10841561		
COMMENT	Contact: Dimopoulos G Fotis C. Kafatos laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany. Location/Qualifiers 1. .1004 /organism="Anopheles gambiae" /mol_type="mRNA" /strain="4A r/r" /db_xref="taxon:7165" /clone="4A3A-P4G8" /cell_line="immune competent 4A3A" /lab_host="E. coli DH10B" /notes="Vector: p7713D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996). Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."		
FEATURES	source		
ORIGIN			
Query Match	15.7%	Score 920.8;	DB 1; Length 1004;
Best Local Similarity	98.8%	Pred. No. 1e-268;	
Matches 999;	Conservative 1;	Mismatches 4;	Indels 7; Gaps 7;
Qy	4023	AAAAGCCAGGAACCGTAAAGGCGCGTTCGTCGGCTTTTCCATAGGCTCCGCCCC	4082
Db	1	AAAAGCCAGGAACCGTAAAGGCGCGTTCGTCGGCTTTTCCATAGGCTCCGCCCC	60
Qy	4083	CTGACGAGCATCAAAATTCAGCTCAAGTCAGAGTGCGCAACCCGACGAGCTAT	4142
Db	61	CTGACGAGCATCAAAATTCAGCTCAAGTCAGAGTGCGCAACCCGACGAGCTAT	120
Qy	4143	AAAAGATACAGGCGTTTCCCGCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGC	4202
Db	121	AAAAGATACAGGCGTTTCCCGCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGC	180
Qy	4203	CGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCT	4262
Db	181	CGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCT	240
Qy	4263	CACGCTGTAGGTATCTCAGTTTCGGTGTAGTTCGTTCCGCTCCAAAGCTGGGCTGTGTGCAG	4322
Db	241	CACGCTGTAGGTATCTCAGTTTCGGTGTAGTTCGTTCCGCTCCAAAGCTGGGCTGTGTGCAG	300
Qy	4323	AACCCCGCTTCAGCCCGACCGCTGCTTATCCGGTAACTATCGTTTGTAGTCCAACC	4382
Db	301	AACCCCGCTTCAGCCCGACCGCTGCTTATCCGGTAACTATCGTTTGTAGTCCAACC	360
Qy	4383	CGGTAAAGACACGACTTATCGCCACTGGCAGCAGCACCTGGTAAACAGGATTAGCAGACGA	4442
Db	361	CGGTAAAGACACGACTTATCGCCACTGGCAGCAGCACCTGGTAAACAGGATTAGCAGACGA	420
Qy	4443	GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGCTACACTAGAA	4502
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Qy	4503	GGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGGAGTTGGTA	4562
Db	481	GAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGGAGTTGGTA	540
Qy	4563	GCTCTTGATCCGGCAAAACCAACACCGCTGCTAGCGGTGGTTTTTTTGTTCGAAGCAGC	4622
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Qy	4623	AGATTACGGCGCAGAAAAAAGGATCTCAAGAAGATCTTTTGATCTTTCTACGGGTCTG	4682
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Qy	4683	ACGCTCAGTGGAAAGAAAACTCAAGTAAAGGATTTGGTCAATGAGATTTATCAAAAAAGA	4742
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Qy	4983	CAGATTATTCAGCAATTAACACGACCGAGCGGAGGCGGAGCGAGCAAGTG	5033
Db	956	CAGATTATTCAGCAATTAACACGACCGAGCGGAGGCGGAGCGAGCAAGTG	1004
RESULT 5			
LOCUS	CO487414	928 bp mRNA linear	EST 09-JUL-2004
DEFINITION	GQ0227.B7.1 K04 GQ022: ROOT XYLEM - mature trees Picea glauca cDNA clone GQ0227.B7_K04 3', mRNA sequence.		
ACCESSION	CO487414		
VERSION	CO487414.1	GI:50174316	
KEYWORDS	EST.		
SOURCE	Picea glauca (white spruce)		
ORGANISM	Picea glauca		
REFERENCE	1 (bases 1 to 928)		
AUTHORS	Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J.,		

Siddiqui, A., Holt, R., Marra, M. and Mackay, J.
 Arborea EST sequencing in *Picea glauca* (white spruce)
 Unpublished (2004)
 Contact: John Mackay
 Centre de Recherche en Biologie Forestiere
 Universite Laval
 Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
 Fax: 418 656 7493
 Email: jmackay@rsvs.ulaval.ca
 Center for Computational Genomics and Bioinformatics (CCGB),
 University of Minnesota, MN id Identifier: WNS286152 Clone ID:
 GQ0227.B7_K04 Clones available through: John Mackay, Ph. D.
 Professor adjoint -Assistant professor EMAIL:
 jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere
 (Forest Biology Research Centre) Universite Laval Quebec, Quebec
 CANADA G1K 7P4

Plate: 7.B7 row: 04 column: K
 Seq primer: T7 Primer.

FEATURES source

1. .928
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 /tissue_type="Differentiating xylem from roots 1 cm in diameter or larger"
 /dev_stage="Non-lignified xylem tissues from larger roots in early part of growing season (June)."
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 /clone_lib="GQ022: ROOT XYLEM - mature trees"
 /notes="Organ: Roots from 9 year old trees measuring approximately 4.5 m tall, and 10 cm in diameter.; Vector: pBluescript II SK (+) XR; Site1: Eco-RI; Site2: Xho-I; cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitro) for propagation"

Query Match 15.1%; Score 886.6; DB 7; Length 928;
 Best Local Similarity 95.8%; Pred. No. 2.8e-258;
 Matches 889; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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 DB 1 TTTTCATAGGCTCGGCCCCCTGACGAGCATCAAAATCGAGCTCAAGTNNNNNN 60

QY 4123 GCGAAACCGCAGAGGACTATAAGATACACAGGGGTTTCCCGCTGGAAGCTCCCTCGTGG 4182
 DB 61 GCGAAACCGCAGAGGACTATAAGATACACAGGGGTTTCCCGCTGGAAGCTCCCTCGTGG 120

QY 4183 CTCTCTGTTCCGACCGCTGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAG 4242
 DB 121 CTCTCTGTTCCGACCGCTGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAG 180

QY 4243 CGTGGCGCTTCTCATGTCTACGCTGTAGTATCTCAGTTCGGTGTAGTTCGCTC 4302
 DB 181 CGTGGCGCTTCTCATGTCTACGCTGTAGTATCTCAGTTCGGTGTAGTTCGCTC 240

QY 4303 CAACTGGGCTGTGTGCAGAACCCCGCTTACCGCGACCGCTGCGCTTATCCGGTAA 4362
 DB 241 CAACTGGGCTGTGTGCAGAACCCCGCTTACCGCGACCGCTGCGCTTATCCGGTAA 300

QY 4363 CTATCGTGTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGCGCAGCAGCACTGG 4422
 DB 301 CTATCGTGTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGCGCAGCAGCACTGG 360

QY 4423 TAACAGGATAGCAGAGCGAGGTATGTAGCGGTGTCTACAGATTCTTGAAGTGGTGGC 4482
 DB 361 TAACAGGATAGCAGAGCGAGGTATGTAGCGGTGTCTACAGATTCTTGAAGTGGTGGC 420

ORIGIN

CR753463 902 bp mRNA linear EST 01-SEP-2004
 DKF2p469G045_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
 DKF2p469G045_5', mRNA sequence.
 CR753463
 CR753463.1 GI:51845874
 EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 REFERENCE 1 (bases 1 to 902)
 AUTHORS Ansorge, W., Krieger, S., Regiert, T., Rittmüller, C., Schwager, B.,
 Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
 Wiemann, S.
 Pongo pygmaeus mRNA (Ansorge, W., Krieger, S., Regiert, T., et al.)
 Unpublished (2004)
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKF2);
 Email s.wiemann@kfz-heidelberg.de; lin, Germany. Please contact
 RZPD for ordering:
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/ci.cgi?CloneID=DKF2p469G045
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES
 source
 1. .902
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 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKF2p469G045"
 /tissue_type="kidney"
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QY 4543 CTTGCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGTTAGCGGTG 4602
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QY 4663 GATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGGATTTTGGT 4722
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QY 4783 ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGA 4842
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QY 4843 GGCACCTATCTCAGCGATCTGCTATTTTCGTTTCATCCATAGTTGCTGACTCCCGCTCGT 4902
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QY 4903 GTAGATAACTAGATACGAGGAGGCTTACATCTGCCCCAGTGTGCAATGATACCGCG 4962
 DB 841 GTNNNTNACTAGNTACGAGGAGGCTTACCANCTGNNNNNNGTGTGCTCAATGATACNGCG 900

QY 4963 AGACCCACGCTCACCGGCTCCAGATTTA 4990
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RESULT 6

CR753463/c
 LOCUS
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

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Query Match		14.9%; Score 876.4; DB 7; Length 902;	
Best Local Similarity		97.7%; Pred. No. 3.7e-255;	
Matches 899; Conservative		0; Mismatches 1; Indels 2; Gaps 2;	
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QY	4966	CCACGCTCACCAGCTCCAGATTATCAGCAATAAACACGACCGCGGAAGGCGCAGCG	5025
Db	841	CCACGCTCACCAGCTCCAGATTATCAGCAATAAACACGACCGCGGAAGGCGCAGCG	782
QY	5026	CAGAGTGTCTGCAACTTTATCCGCCCTCCATCCAGTCTATTAAATGTTGCGGGAAGC	5085
Db	781	CAGAGTGTCTGCAACTTTATCCGCCCTCCATCCAGTCTATTAAATGTTGCGGGAAGC	722
QY	5086	TAGAGTAAGTAGTTCGCCAGTTTAATAGTTTGGCAACGTTGTTGCCATTGCTACAGGCAT	5145
Db	721	TAGAGTAAGTAGTTCGCCAGTTTAATAGTTTGGC- AAGGTTGTTGCCATTGCTACAGGCAT	663
QY	5146	CGTGTGTACCGTCTGCTGTTGGTATGCGTTCATTCAGCTCGGTTCCCAACGATCAAG	5205
Db	662	CGTGTGTACCGTCTGCTGTTGGTATGCGTTCATTCAGCTCGGTTCCCAACGATCAAG	603
QY	5206	GGAGTTCATATCCCCATGTTGTGCAAAAAGCGGTTAGCTCTTCGGTCTCCGAT	5265
Db	602	GGAGTTCATATCCCCATGTTGTGCAAAAAGCGGTTAGCT-CTTCGGTCTCCGAT	544
QY	5266	CGTTGTGAGAAGTAAGTTGGCGCGAGTTTATCACTCATGTTATGGCAGCACTGCATAA	5325
Db	543	CGTTGTGAGAAGTAAGTTGGCGCGAGTTTATCACTCATGTTATGGCAGCACTGCATAA	484
QY	5326	TTCTCTTACTGATGCGATCCGTAAGATGCTTTTCTGTGACTGTGTGATCTACACCAA	5385
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QY	5386	GTCAATTCAGAAATAGTGTACGGCGACCGAGTTGCTCTCCCGCGGTCAATACGGGA	5445
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QY	5446	TAATACCGCGCACATPAGCAGAACTTTAAAAGTGTCTCATCATTTGGAAAAACGTTCTTCGGG	5505
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QY	5506	GGGAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAAACCACTCGTGC	5565
Db	303	GGGAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAAACCACTCGTGC	244
QY	5566	ACCCAACTCATCTCAGCATCTTTTACTTTTACACGAGCTTCTGGGTGAGCAAAACAGG	5625
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QY	5746	ATTGTGAATCTATTAGAAAAATAAACAAATAGGGGTTCCGCGACATTTTCCCGGAAAGT	5805
Db	63	ATTGTGAATCTATTAGAAAAATAAACAAATAGGGGTTCCGCGACATTTTCCCGGAAAGT	4
QY	5806	GC 5807	
Db	3	GC 2	

RESULT 7		BG838279/c		935 bp		mRNA		linear		EST 25-MAY-2001	
LOCUS		Gc01_10e07_R Gc01_AAF		ECORC_cold_stressed		Glycine_clandestina					
DEFINITION		Glycine clandestina cDNA clone Gc01_10e07,		mRNA sequence.							
ACCESSION		BG838279									
VERSION		BG838279.1		GI:14204601							
KEYWORDS		EST.									
ORGANISM		Glycine clandestina									
REFERENCE		1 (bases 1 to 935)									
AUTHORS		Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.									
TITLE		Expressed Sequence Tags from Cold-Stressed Glycine clandestina Seedlings									
JOURNAL		Unpublished (2001)									
COMMENT		Contact: Singh,J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada Tel: (613) 759-1662 Fax: (613) 759-1701 Email: singhja@agr.gc.ca.									
FEATURES		Location/Qualifiers									
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ORIGIN											
Query Match		14.9%; Score 875.8; DB 4; Length 935;									
Best Local Similarity		97.7%; Pred. No. 5.6e-255;									
Matches 882; Conservative		14; Mismatches 6; Indels 1; Gaps 1;									
QY	4921	GGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAGAGCCACCGTCAACCGGC	4980								
Db	928	GGGGGGCTTACCATCTGCCCCAGTGTGCAATGATACCGGAGAGCCACCGTCAACCGGC	869								
QY	4981	TCCAGATTATCAGCAATAAACCGACCGGAGGCGCGGAGGAGGAGGAGGAGGAGGAGG	5040								
Db	868	YCCAGATTATCAGCAATAAACCCACCGCGGAGGCGCGGAGGAGGAGGAGGAGGAGGAGG	809								
QY	5041	AACTTTATCCGCTCCATCCAGTCTATTAAATGTTTGGCGGGAAGCTAGAGTAAGTAGTTC	5100								
Db	808	AWCTTTATCCGCGCTCCATCCAGTCTATTAAATGTTTGGCGGGAAGCTAGAGTAAGTAGTTC	749								
QY	5101	GCCAGTTAATAGTTTGGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCAAGCTC	5160								
Db	748	GCCAGTTAATAGTTTGGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCAAGCTC	689								
QY	5161	GTCTGTTGTATGGCTTCATTCAGCTCCGGTTCCTCCCAACGATCAAGGCGAGTTACATGATC	5220								
Db	688	GTCTGTTGTATGGCTTCATTCAGCTCCGGTTCCTCCCAACGATCAAGGCGAGTTACATGATC	629								
QY	5221	CCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCTCTCCGATCGTTGTTCAGAGTAA	5280								

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Db 628 CCCCATGTTGTGCAAAAAGCGTTAGCTCTTCGGTCTCCGATCGTTGTCAGAAAGTAA 569
Qy 5281 GTT-GGCGGAGGTTATCACTCATGTTATGCGACACGACATGCTCTTACTGTCA 5339
Db 568 GTTGGGCGGAGGTTATCACTCATGTTATGCGACACGACATGCTCTTACTGTCA 509
Qy 5340 TGCCATCCGTAAGATGCTTTTCTGTGACTGTTGAGTACTCAACCAAGTCAATCTGAGAAT 5399
Db 508 TGCCATCCGTAAGATGCTTTTCTGTGACTGTTGAGTACTCAACCAAGTCAATCTGAGAAT 449
Qy 5400 AGTGTATGCGGCGACGAGTGTCTTTCGCCGGCGTCAATACGGGATAATACGCGGCCAC 5459
Db 448 AGTGTATGCGGCGACGAGTGTCTTTCGCCGGCGTCAATACGGGATAATACGCGGCCAC 389
Qy 5460 ATAGCAGAACTTTAAAGTCTCATATTCGAAAGCTTCTTCGGGGCGAAACTCTCAA 5519
Db 388 ATAGCAGAACTTTAAAGTCTCATATTCGAAAGCTTCTTCGGGGCGAAACTCTCAA 329
Qy 5520 GGATCTTACCGCTTTGAGATCCAGTTCGATGTAACCCACTCGTGACCCAACTGATCTT 5579
Db 328 GGATCTTACCGCTTTGAGATCCAGTTCGATGTAACCCACTCGTGACCCAACTGATCTT 269
Qy 5580 CAGCATCTTTTACTTTTACAGCGTTTCTGGGTGAGCAAAAACAGGAGGCAAAATGCCG 5639
Db 268 CAGCATCTTTTACTTTTACAGCGTTTCTGGGTGAGCAAAAACAGGAGGCAAAATGCCG 209
Qy 5640 CAAAAAGGGAATAAGGGGACACGGAATGTTGAATCTCATCTCTTCTTTTCAAT 5699
Db 208 CAAAAAGGGAATAAGGGGACACGGAATGTTGAATCTCATCTCTTCTTTTCAAT 149
Qy 5700 ATATTGAAGCAATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGATTT 5759
Db 148 ATATTGAAGCAATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGATTT 89
Qy 5760 AGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAGTGCCACCTGAGCTCT 5819
Db 88 AGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAGTGCCACCTGAGCTCT 29
Qy 5820 AAG 5822
Db 28 AAG 26

RESULT 8
AL042026/c
LOCUS      841 bp      mRNA      linear      EST 04-SEP-2003
DEFINITION DKFZp434E111_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION  AL042026
VERSION     AL042026.1 GI:5421372
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 841)
AUTHORS   Poustka A., Klein M., Mewes H.W., Gassenhuber J. and Wiemann S.
TITLE     EST (Poustka, et al.)
JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            Heidelberg/DKFZ (German Cancer Research Center,
            German Genome Project.
            No sl sequence available.
            This clone (DKFZp434E111) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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FEATURES
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Location/Qualifiers
1..841
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/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      14.3%; Score 841; DB 1; Length 841;
Best Local Similarity 100.0%; Pred. No. 2.3e-244;
Matches 841; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4936 TGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTCACCGGTCCAGATTATCAGC 4995
Db 841 TGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTCACCGGTCCAGATTATCAGC 782
Qy 4996 AATAAACACGAGCCGAGGAGGCGGAGGAGTGGTCTCTGCAACTTTATCCGCTC 5055
Db 781 AATAAACACGAGCCGAGGAGGCGGAGGAGTGGTCTCTGCAACTTTATCCGCTC 722
Qy 5056 CATCCAGTCTATTAAATGTTTGGCGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTT 5115
Db 721 CATCCAGTCTATTAAATGTTTGGCGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTT 662
Qy 5116 GGGCAAGTGTGTCATTGCTACAGGCAATCGTGGTGTACGCTCGTCTGTTGGTATGGC 5175
Db 661 GGGCAAGTGTGTCATTGCTACAGGCAATCGTGGTGTACGCTCGTCTGTTGGTATGGC 602
Qy 5176 TTCAATTCAGTCCGGTTCCTCCAGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAA 5235
Db 601 TTCAATTCAGTCCGGTTCCTCCAGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAA 542
Qy 5236 AAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTGTGTGAGAAGTAAGTGGCCGAGTGT 5295
Db 541 AAAAGCGGTTAGTCTCTCGGTCCTCCGATCGTGTGTGAGAAGTAAGTGGCCGAGTGT 482
Qy 5296 ATCACTCATGTTTANGGAGCACTGCATAAATCTCTTATCTGTATGTCATGCGCAATG 5355
Db 481 ATCACTCATGTTTANGGAGCACTGCATAAATCTCTTATCTGTATGTCATGCGCAATG 422
Qy 5356 CTTTCTGTGACTGGTGTGACTCTCAACCAAGTCAATCTGAGATAGTGTATGCGGAC 5415
Db 421 CTTTCTGTGACTGGTGTGACTCTCAACCAAGTCAATCTGAGATAGTGTATGCGGAC 362
Qy 5416 GAGTGTCTCTTGGCCGCGCTCAATACGGGATATATACCGGCCACATAGCAGAACTTTAAA 5475
Db 361 GAGTGTCTCTTGGCCGCGCTCAATACGGGATATATACCGGCCACATAGCAGAACTTTAAA 302
Qy 5476 AGTGTCTCATCTATGGAAAACGTTCTTTCGGGGGAAAACCTCTCAAGGATCTTACCGTGT 5535
Db 301 AGTGTCTCATCTATGGAAAACGTTCTTTCGGGGGAAAACCTCTCAAGGATCTTACCGTGT 242
Qy 5536 GAGATCCAGTTCGATGTAAACCACTCGTGCACCCCACTGATCTTCAGCATCTTTTACTTT 5595
Db 241 GAGATCCAGTTCGATGTAAACCACTCGTGCACCCCACTGATCTTCAGCATCTTTTACTTT 182
Qy 5596 CACCAGCGTTTCTGGGTGAGCAAAAACAGGAGGCAAAATGCGGCAAAAAGGGAATAAG 5655
Db 181 CACCAGCGTTTCTGGGTGAGCAAAAACAGGAGGCAAAATGCGGCAAAAAGGGAATAAG 122
Qy 5656 GCGCACACGAAAATGTTGAATACTCATCTCTTCTTTTCAATATATTATGAAGCAATTA 5715
Db 121 GCGCACACGAAAATGTTGAATACTCATCTCTTCTTTTCAATATATTATGAAGCAATTA 62
Qy 5716 TCAGGGTTATTGTCTCATGAGCGGATACATATTTTGAATGATTTTGAATAATAACAAAT 5775
Db 61 TCAGGGTTATTGTCTCATGAGCGGATACATATTTTGAATGATTTTGAATAATAACAAAT 2
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NotI; 0-10 DAF (days after flowering), cDNA synthesis  
using pBluescript II XR cDNA-library construction kit  
(Stratagene) with an oligo(dT)-primer containing NotI  
restriction site and a Sali adapter (Invitrogen). The main  
library of 21500 clones was rearayed into the sublibrary  
BES 1824 containing 4100 putative expression clones. Note:  
Due to a cloning artefact caused by the kit, in most cases  
the Sali site is NOT present, as well as the Sali Adapter  
used for cloning. To excise the insert, restriction sites  
upstream Sali should be used (e.g. BamHI). Average insert  
size is 1 kb. Library generation and sequencing was  
granted in context of GABI; data are also accessible at  
https://gabi.rzpd.de"
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ORIGIN

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Query Match 13.9%; Score 817; DB 7; Length 865;  
Best Local Similarity 98.0%; Pred. No. 5.1e-237;  
Matches 847; Conservative 0; Mismatches 13; Indels 4; Gaps 2;  
  
QY 3905 TCCTGGCTCGCTCGTTCGGCTGCGGAGCGGTATCAGTCACTCAAGGGCGTAATA 3964  
DB 1 TCCTGGCTCGTTCGGCTGCGGAGCGGTATCAGTCACTCAAGGGCGTAATA 60  
  
QY 3965 CGGTTATCCACAGATCAGGGGATAACGAGGAAAGAACATGAGCAAAAGGCCAGCA 4024  
DB 61 CGGTTATCCACAGATCAGGGGATAACGAGGAAAGAACATGAGCAAAAGGCCAGCA 120  
  
QY 4025 AAGGCCAGGAACCGTAAAAAGCGCGTTCCTGGCGTTTTCATAGGCTCCGCCCCCT 4084  
DB 121 AAGGCCAGGAACCGTAAAAAGCGCGTTCCTGGCGTTTTCATAGGCTCCGCCCCCT 180  
  
QY 4085 GACGAGATCAGAAAATCAGCGCTCAAGTCAGAGTGGGGAACCGCAGAGACTATAA 4144  
DB 181 GACGAGATCAGAAAATCAGCGCTCAAGTCAGAGTGGGGAACCGCAGAGACTATAA 240  
  
QY 4145 AGATACAGCGCTTCCCTCGTGAAGCTCCCTCGTGCGCTCTCCTGTTCGACCTGCCG 4204  
DB 241 AGATACAGCGCTTCCCTCGTGAAGCTCCCTCGTGCGCTCTCCTGTTCGACCTGCCG 300  
  
QY 4205 CTTACCGGATACCTGTCGCTTTCCTTCGCGAAGCGTGGCGTTCCTCAATGCTCA 4264  
DB 301 CTTACCGGATACCTGTCGCTTTCCTTCGCGAAGCGTGGCGTTCCTCAATGCTCA 360  
  
QY 4265 CGCTGTAGGTATCTCAGTTCGGTGTAGGTCTTCCTCCAGCTGGGCTGTGTGCAGAA 4324  
DB 361 CGCTGTAGGTATCTCAGTTCGGTGTAGGTCTTCCTCCAGCTGGGCTGTGTGCAGAA 420  
  
QY 4325 CCCCCCGTTCCAGCCGCGCTCGCTTTCGGAAGTATCGTCTTGAAGTCCACCCG 4384  
DB 421 CCCCCCGTTCCAGCCGCGCTCGCTTTCGGAAGTATCGTCTTGAAGTCCACCCG 480  
  
QY 4385 GTAAGACACGACTATTCGCGCACTGGCAGCAGCCACTGGTAAACAGGATTCAGAGCGAGG 4444  
DB 481 GTAAGACACGACTATTCGCGCACTGGCAGCAGCCACTGGTAAACAGGATTCAGAGCGAGG 540  
  
QY 4445 TATGTAGCGGCTACAGAGTCTTGAAGTGGTGGCTTAACCTACCGCTACCTAGAGG 4504  
DB 541 TATGTAGCGGCTACAGAGTCTTGAAGTGGTGGCTTAACCTACCGCTACCTAGAGG 600  
  
QY 4505 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCGAGTACCTTCGGAAGAGTGTGTAGC 4564  
DB 601 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCGAGTACCTTCGGAAGAGTGTGTAGC 660  
  
QY 4565 TCTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTTCAGAGCAGCAG 4624
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DB 661 TCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTTTGTTCAGACGACAG 720  
QY 4625 ATTACCGGAGAAAAAGGATCTCAAGAGATCCCTTGTGATCTTCTACGGGTCTGAC 4684  
DB 721 ATTACCGGAGAAAAAGGATCTCAAGAGATCCCTTGTGATCTTCTACGGGTCTGAC 780  
QY 4685 GCTCAGTGGAAACCAAACTCACGTT--AAGGGATTTTGGTCAATGA--GATTATCAAAAAG 4740  
DB 781 GCTCAGTGGAAACCAAACTCACGTTTAAACGGGATTTTGGTCAATGAATATCAAAAAG 840  
QY 4741 GATCTTCACCTAGATCTTTTAA 4764  
DB 841 GATCTTCACCTANATCTTTTAA 864  
  
RESULT 11  
BZ577702/c  
LOCUS  
DEFINITION  
1126 bp DNA linear GSS 17-DEC-2002  
msh2 5533.Y2 msh Pseudomonas aeruginosa genomic clone msh2_5533,  
genomic survey sequence.  
ACCESSION  
BZ577702  
VERSION  
BZ577702.1  
KEYWORDS  
GSS.  
SOURCE  
Pseudomonas aeruginosa  
ORGANISM  
Pseudomonas aeruginosa  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.  
REFERENCE  
1 (bases 1 to 1126)  
AUTHORS  
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,  
Burns,J.L., Kaul,R. and Olsen,M.V.  
TITLE  
Whole-Genome-Sequence variation among multiple isolates of  
Pseudomonas aeruginosa library  
JOURNAL  
J. Bacteriol. (2002) In press  
COMMENT  
Contact: Chris K. Raymond  
Genome Center  
University of Washington  
Box 352145, Seattle, WA 98105-2145, USA  
Tel: 2062216954  
Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun.  
Location/Qualifiers  
1..1126  
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/strain="WSH"  
/db_xref="taxon:287"  
/clone="msh2_5533"  
/clone_lib="msh"  
/notes="Environmental isolate. Whole genomic shotgun  
library."  
  
ORIGIN  
  
Query Match 13.8%; Score 814.4; DB 8; Length 1126;  
Best Local Similarity 90.4%; Pred. No. 3.5e-236;  
Matches 938; Conservative 0; Mismatches 91; Indels 9; Gaps 6;  
  
QY 4735 AAAAGGATCTCCCTAGATCCCTTTTAAATTAATAAAGTAAATCAATCTAAAG 4794  
DB 1125 AAAAGGTTCTTCCCTAGACCCCTT--AATAAAGAAAGTTTAAATCAATTTAAG 1069  
QY 4795 TATATATAGTAACCTTGGTCTGACAGTTACCAATGTTTAAATCAATGAGGCACC-TATCT 4853  
DB 1068 --TATTGAGTAACTTGTTCGACAGTGTCAAAGTTATATCATGAAGCCCCCTTATCA 1011  
QY 4854 CAGCATCTGTCTATTTTCGTTTATCC-ATAGTTGCTGACTCCCC-GTCGTGTAGATAAC 4911  
DB 1010 AGCTATCTGTCTATTTTCGTTTAAACAATAGTTCCCTGACTCCCGTCCGGTAGAAT 951  
QY 4912 TACGATACGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAGACCCAG 4971  
DB 950 TCCGATCGGAGGGTTTCTTATTTGCCCCCAAGTAGTCAATGTAAACCGGAGCCCCCG 891
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QY	4972	CTCACGGCTCCAGATTTATCAGCAATAAACACAGCCAGCCGAGGGCCGAGCGAGAG	5031
DB	890	TTCCCGCGCTCCAATTTATCCCAATAACCAAGCATCCGAAAGGGCCGAGCCCAAAAG	831
QY	5032	TGTCCTCGCAAC-TTTATCGGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAG	5090
DB	830	TGGTCTCGCAACTTTTATCAGCTCCATCAGTCTATTAATTGTTGCCGGGAAGCTAGAG	771
QY	5091	TAAGTAGTTCCGCAAGTAATAGTTTTCGCAACAGTTGTTGCCATGCTACAGGCACTGCG	5150
DB	770	TCAGTAGTTCCGCAAGTAATAGTAGTATGCGCAACGTTGTTGCCATGCTACAGGCACTGCG	711
QY	5151	TGTCAGCTCGCTGTTGGTATGGCTTCAATCAGCTCCGTTCCCAACATCAAGGCGAG	5210
DB	710	TGTCAAGCTGGTGGTATGGCTTCAATCAGCTCCGTTCCCAACATCAAGGCGAG	651
QY	5211	TTACATGATCCCCCATGTTGTGCAAAAAGCGTTAGCTCCTTCCGTCCTCCGATCGTTG	5270
DB	650	TTACATGATCCGCGATGTTGTGCAAAAAGCGTTAGCTCCTTCCGTCCTCCGATCGTTG	591
QY	5271	TCAGAAGTAAGTTGGCGGAGTGTATCACTCATGTTATGGCAGCACTGCAATAATTCTC	5330
DB	590	TCATAAGTAAGTTGACCGCAGTGTATCACTCATGTTATGGCAGCACTGCAATAATTCTC	531
QY	5331	TTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGATGCTGAGTACTCAACCAAGTCAT	5390
DB	530	TTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGATGCTGAGTACTCAACCAAGTCAT	471
QY	5391	TCGAGAAATAGTATGCGCGACCGAGTTGCTCTTCCGCGCTCAATACGGGATAATA	5450
DB	470	TCGAGAAATAGTATGCGCGACCGAGTTGCTCTTCCGCGCTCAATACGGGATAATA	411
QY	5451	CCGCGCCACATAGCAGAACTTTAAAAAGTGCTCATCATTTGGAATAAGTCTTCCGCGCGAA	5510
DB	410	CCGCGCCACATAGCAGAACTTTAAAAAGTGCTCATCATTTGGAATAAGTCTTCCGCGCGAA	351
QY	5511	AACTCTCAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAAACCCACTCGTGACCCA	5570
DB	350	AACTCTCAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAAACCCACTCGTGACCCA	291
QY	5571	ACTGATCTTTCAGCATCTTTTACTTTTCCAGCGTTTCTCGGTGAGCAAAAACAGGAAGC	5630
DB	290	ACTGATCTTTCAGCATCTTTTACTTTTCCAGCGTTTCTCGGTGAGCAAAAACAGGAAGC	231
QY	5631	AAATGCCCAAAAAGGAATAAGGGCGACACGGAAATGTTGAAATCTCATCTCTTCC	5690
DB	230	AAATGCCCAAAAAGGAATAAGGGCGACACGGAAATGTTGAAATCTCATCTCTTCC	171
QY	5691	TTTTTCAATATTATGAAGCATTTATCAGGTTTATGTCATGAGCGGATACATATTG	5750
DB	170	TTTTTCAATATTATGAAGCATTTATCAGGTTTATGTCATGAGCGGATACATATTG	111
QY	5751	AATGTAATTTAGAAAAATA	5768
DB	110	AATGTAATTTAGAAAAATA	93

RESULT 12
CN823189/c
LOCUS
DEFINITION
Oa_splbn_06L10_M13reverse Sheep spleen\brain pSport1 library Ovis
arles cDNA clone Oa_splbn_06L10 5', mRNA sequence.
CN823189
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ovis aries (sheep)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
1 (bases 1 to 856)
REFERENCE
AUTHORS
Gosner,A. and Hopkins,J.

TITLE
JOURNAL
COMMENT
Ovine spleen\brain cDNA library
Unpublished (2004)
Contact: J Hopkins
Veterinary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1QH.
Email: j.hopkins@ed.ac.uk
Plate: 06 row: L column: 10
Seq primer: M13reverse
High quality sequence start: 6
High quality sequence stop: 548.
FEATURES
Location/Qualifiers
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ORIGIN

Query Match	13.8%;	Score	809.4;	DB	7;	Length	856;
Best Local Similarity	98.0%;	Pred. No.	1.1e-234;				
Matches	830;	Conservative	0;	Mismatches	16;	Indels	1;
Gaps	1;						
QY	4964	GA	CC	CA	CG	CT	CA
DB	856	GA	CC	CA	CG	CT	CA
QY	5024	CG	CA	GA	AG	TG	GT
DB	797	CG	CA	GA	AG	TG	GT
QY	5084	GC	TA	GA	TA	AG	TA
DB	737	GC	TA	GA	TA	AG	TA
QY	5144	AT	CG	TG	GT	CA	CG
DB	677	AT	CG	TG	GT	CA	CG
QY	5204	AG	CG	CA	GT	TT	CG
DB	617	AG	CG	CA	GT	TT	CG
QY	5264	AT	CG	TG	GT	CA	CG
DB	557	AT	CG	TG	GT	CA	CG
QY	5324	AA	TT	CT	CT	TA	CT
DB	497	AA	TT	CT	CT	TA	CT
QY	5384	AA	GT	CA	TT	CT	CA
DB	437	AA	GT	CA	TT	CT	CA
QY	5444	GA	TA	TA	TA	TA	TA
DB	377	GA	TA	TA	TA	TA	TA
QY	5504	GG	CG	CA	AA	CT	CG
DB	317	GG	CG	CA	AA	CT	CG
QY	5564	GC	AC	CA	CT	CT	CA
DB	257	GC	AC	CA	CT	CT	CA
QY	5624	GA	AG	CG	CA	AA	AG
DB	197	GA	AG	CG	CA	AA	AG

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QY 5684 CTCTTCTTTTCAATATATTAAGCATTTATCAGGGTTATTGTCTCATGACGGATAC 5743
Db 137 CTCTTCTTTTCAATATATTAAGCATTTATCAGGGTTATTGTCTCATGACGGATAC 78
QY 5744 ATATTTGAATGTTTATAGAAAATAAACAATAGGGTTCCGGCGACATTTCCCGAATA 5803
Db 77 ATATTTGAATGTTTATAGAAAATAAACAATAGGGTTTTCGACCGGGAATCCGACCG 18
QY 5804 GTGCCAC 5810
Db 17 GTACCGC 11

RESULT 13
CD649375/c
LOCUS Crassostrea virginica Gonad Crassostrea virginica cDNA
DEFINITION 5', mRNA sequence.
ACCESSION CD649375
VERSION CD649375.1 GI:31906346
KEYWORDS EST.
SOURCE Crassostrea virginica (eastern oyster)
ORGANISM Crassostrea virginica
REFERENCE 1 (bases 1 to 819)
AUTHORS Peatman,E., Kucuktas,H., Li,P., He,C., Feng,J., Wei,X. and Liu,Z.
TITLE Differentially expressed oyster (Crassostrea virginica) genes after
exposure to mercury
JOURNAL Unpublished (2003)
COMMENT Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
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/organism="Crassostrea virginica"
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/clone_lib="Crassostrea virginica Gonad"
/notes="Organ: Gonad; Vector: pSport1; Site_1: NotI;
Site_2: SalI"
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Query Match 13.7%; Score 808; DB 6; Length 819;
Best Local Similarity 99.9%; Pred.No.2.8e-234;
Matches 819; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 4818 ACAGTTTACCAATGCTTAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTCGTTTCA 4877
Db 819 ACAGTTTACCAATGCTTAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTCGTTTCA 760
QY 4878 CCATAGTTGCTGACCTCCCGTCTGTAGATACTAGATACGGAGGGCTTACCATCTG 4937
Db 759 CCATAGTTGCTGACCTCCCGTCTGTAGATACTAGATACGGAGGGCTTACCATCTG 700
QY 4938 GCCCCAGTGTGCAATGATACCGGAGACCCAGCTCACCGGCTCCAGATTATACGAA 4997
Db 699 GCCCCAGTGTGCAATGATACCGGAGACCCAGCTCACCGGCTCCAGATTATACGAA 640
QY 4998 TAAACAGCCAGCCGGAAGGCCGAGCGCAGAGAGTGTCTCGCAACTTTATCCGCTCCA 5057
Db 639 TAAACAGCCAGCCGGAAGGCCGAGCGCAGAGAGTGTCTCGCAACTTTATCCGCTCCA 580
QY 5058 TCAGTCTATTATTTGTCGGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTC 5117
Db 579 TCAGTCTATTATTTGTCGGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTC 520
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QY 5118 GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCAAGCTCGTCTGTTGGTATGCTTT 5177
Db 519 GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCAAGCTCGTCTGTTGGTATGCTTT 460
QY 5178 CATTCAGCTCCGGTTCCTCCAAACGATCAAGCGAGTTACATGATCCCCCATGTTGTCAGAAA 5237
Db 459 CATTCAGCTCCGGTTCCTCCAAACGATCAAGCGAGTTACATGATCCCCCATGTTGTCAGAAA 400
QY 5238 AAGCGGTTAGCTCCTTCGGTCTCCGATCGTGTGTGAGAGTAGTGTGGCCGCGAGTGTAT 5297
Db 399 AAGCGGTTAGCT-CITTCGGTCTCCGATCGTGTGTGAGAGTAGTGTGGCCGCGAGTGTAT 341
QY 5298 CACTCATGTTATGGCAGCACTGCATAATTCTCTTACTGTCTATGCCATCCGTAAGATGCT 5357
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VERSION BZ576726.1 GI:27211787
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
REFERENCE 1 (bases 1 to 1011)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
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/note="Environmental isolate. Whole genomic shotgun"
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